SEQUENCE LISTING

<110> Vander Horn, Peter B.
      MJ Bioworks, Inc.

<120> Methods of Making Hybrid Proteins

<130> 020130-001420US

<140> US 10/627,592
<141> 2003-07-25

<150> US 60/463,781
<151> 2003-04-17

<150> US 60/483,287
<151> 2003-06-27

<160> 50

<170> PatentIn Ver. 2.1

<210> 1
<211> 493
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:BlastP
      alignment Pyrococcus furiosus DNA polymerase (Pfu)
      query sequence

<400> 1
Met Ile Leu Asp Val Asp Tyr Ile Thr Glu Glu Gly Lys Pro Val Ile
 1   5   10   15

Arg Leu Phe Lys Lys Glu Asn Gly Lys Phe Lys Ile Glu His Asp Arg
            20   25   30

Thr Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Arg Asp Asp Ser Lys Ile
        35   40   45

Glu Glu Val Lys Lys Ile Thr Gly Glu Arg His Gly Lys Ile Val Arg
    50   55   60

Ile Val Asp Val Glu Lys Val Glu Lys Lys Phe Leu Gly Lys Pro Ile
65   70   75   80

Thr Val Trp Lys Leu Tyr Leu Glu His Pro Gln Asp Val Pro Thr Ile
                85   90   95

Arg Glu Lys Val Arg Glu His Pro Ala Val Val Asp Ile Phe Glu Tyr
            100   105   110

Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro
        115   120   125

Met Glu Gly Glu Glu Glu Leu Lys Ile Leu Ala Phe Asp Ile Glu Thr
    130   135   140

1

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Leu Tyr His Glu Gly Glu Glu Phe Gly Lys Gly Pro Ile Ile Met Ile
145              150              155              160

Ser Tyr Ala Asp Glu Asn Glu Ala Lys Val Ile Thr Trp Lys Asn Ile
              165              170              175

Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile Lys
              180              185              190

Arg Phe Leu Arg Ile Ile Arg Glu Lys Asp Pro Asp Ile Ile Val Thr
          195              200              205

Tyr Asn Gly Asp Ser Phe Asp Phe Pro Tyr Leu Ala Lys Arg Ala Glu
    210              215              220

Lys Leu Gly Ile Lys Leu Thr Ile Gly Arg Asp Gly Ser Glu Pro Lys
225              230              235              240

Met Gln Arg Ile Gly Asp Met Thr Ala Val Glu Val Lys Gly Arg Ile
              245              250              255

His Phe Asp Leu Tyr His Val Ile Thr Arg Thr Ile Asn Leu Pro Thr
              260              265              270

Tyr Thr Leu Glu Ala Val Tyr Glu Ala Ile Phe Gly Lys Pro Lys Glu
          275              280              285

Lys Val Tyr Ala Asp Glu Ile Ala Lys Ala Trp Glu Ser Gly Glu Asn
    290              295              300

Leu Glu Arg Val Ala Lys Tyr Ser Met Glu Asp Ala Lys Ala Thr Tyr
305              310              315              320

Glu Leu Gly Lys Glu Phe Leu Pro Met Glu Ile Gln Leu Ser Arg Leu
              325              330              335

Val Gly Gln Pro Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu
          340              345              350

Val Glu Trp Phe Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Val Ala
          355              360              365

Pro Asn Lys Pro Ser Glu Glu Glu Tyr Gln Arg Arg Leu Arg Glu Ser
    370              375              380

Tyr Thr Gly Gly Phe Val Lys Glu Pro Glu Lys Gly Leu Trp Glu Asn
385              390              395              400

Ile Val Tyr Leu Asp Phe Arg Ala Leu Tyr Pro Ser Ile Ile Ile Thr
              405              410              415

His Asn Val Ser Pro Asp Thr Leu Asn Leu Glu Gly Cys Lys Asn Tyr
              420              425              430

Asp Ile Ala Pro Gln Val Gly His Lys Phe Cys Lys Asp Ile Pro Gly
          435              440              445

Phe Ile Pro Ser Leu Leu Gly His Leu Leu Glu Glu Arg Gln Lys Ile
    450              455              460
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2

Lys Thr Lys Met Lys Glu Thr Gln Asp Pro Ile Glu Lys Ile Leu Leu
465   470   475   480

Asp Tyr Arg Gln Lys Ala Ile Lys Leu Leu Ala Asn Ser
                485   490

<210> 2
<211> 283
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:BlastP
      alignment Pyrococcus furiosus DNA polymerase (Pfu)
      query sequence

<400> 2
Asn Ser Phe Tyr Gly Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys
  1   5   10   15

Lys Glu Cys Ala Glu Ser Val Thr Ala Trp Gly Arg Lys Tyr Ile Glu
            20   25   30

Leu Val Trp Lys Glu Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr
        35   40   45

Ile Asp Thr Asp Gly Leu Tyr Ala Thr Ile Pro Gly Gly Glu Ser Glu
    50   55   60

Glu Ile Lys Lys Lys Ala Leu Glu Phe Val Lys Tyr Ile Asn Ser Lys
 65   70   75   80

Leu Pro Gly Leu Leu Glu Leu Glu Tyr Glu Gly Phe Tyr Lys Arg Gly
                85   90   95

Phe Phe Val Thr Lys Lys Arg Tyr Ala Val Ile Asp Glu Glu Gly Lys
            100   105   110

Val Ile Thr Arg Gly Leu Glu Ile Val Arg Arg Asp Trp Ser Glu Ile
        115   120   125

Ala Lys Glu Thr Gln Ala Arg Val Leu Glu Thr Ile Leu Lys His Gly
    130   135   140

Asp Val Glu Glu Ala Val Arg Ile Val Lys Glu Val Ile Gln Lys Leu
145   150   155   160

Ala Asn Tyr Glu Ile Pro Pro Glu Lys Leu Ala Ile Tyr Glu Gln Ile
                165   170   175

Thr Arg Pro Leu His Glu Tyr Lys Ala Ile Gly Pro His Val Ala Val
            180   185   190

Ala Lys Lys Leu Ala Ala Lys Gly Val Lys Ile Lys Pro Gly Met Val
        195   200   205

Ile Gly Tyr Ile Val Leu Arg Gly Asp Gly Pro Ile Ser Asn Arg Ala
    210   215   220

3

Ile Leu Ala Glu Glu Tyr Asp Pro Lys Lys His Lys Tyr Asp Ala Glu
225   230   235   240

Tyr Tyr Ile Glu Asn Gln Val Leu Pro Ala Val Leu Arg Ile Leu Glu
                245   250   255

Gly Phe Gly Tyr Arg Lys Glu Asp Leu Arg Tyr Gln Lys Thr Arg Gln
                260   265   270

Val Gly Leu Thr Ser Trp Leu Asn Ile Lys Lys
        275   280

<210> 3
<211> 493
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:BlastP
      alignment Pyrococcus sp. GB-D DNA polymerase (Deep
      Vent) subject sequence

<400> 3
Met Ile Leu Asp Ala Asp Tyr Ile Thr Glu Asp Gly Lys Pro Ile Ile
  1   5   10   15

Arg Ile Phe Lys Lys Glu Asn Gly Glu Phe Lys Val Glu Tyr Asp Arg
            20   25   30

Asn Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Lys Asp Asp Ser Gln Ile
        35   40   45

Asp Glu Val Arg Lys Ile Thr Ala Glu Arg His Gly Lys Ile Val Arg
    50   55   60

Ile Ile Asp Ala Glu Lys Val Arg Lys Lys Phe Leu Gly Arg Pro Ile
 65   70   75   80

Glu Val Trp Arg Leu Tyr Phe Glu His Pro Gln Asp Val Pro Ala Ile
                85   90   95

Arg Asp Lys Ile Arg Glu His Ser Ala Val Ile Asp Ile Phe Glu Tyr
            100   105   110

Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro
        115   120   125

Met Glu Gly Asp Glu Glu Leu Lys Leu Leu Ala Phe Asp Ile Glu Thr
    130   135   140

Leu Tyr His Glu Gly Glu Glu Phe Ala Lys Gly Pro Ile Ile Met Ile
145   150   155   160

Ser Tyr Ala Asp Glu Glu Glu Ala Lys Val Ile Thr Trp Lys Lys Ile
                165   170   175

Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile Lys
            180   185   190

4

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Arg Phe Leu Lys Val Ile Arg Glu Lys Asp Pro Asp Val Ile Ile Thr
    195                     200                 205

Tyr Asn Gly Asp Ser Phe Asp Leu Pro Tyr Leu Val Lys Arg Ala Glu
    210                 215                 220

Lys Leu Gly Ile Lys Leu Pro Leu Gly Arg Asp Gly Ser Glu Pro Lys
225                 230                 235                 240

Met Gln Arg Leu Gly Asp Met Thr Ala Val Glu Ile Lys Gly Arg Ile
            245                 250                 255

His Phe Asp Leu Tyr His Val Ile Arg Arg Thr Ile Asn Leu Pro Thr
            260                 265                 270

Tyr Thr Leu Glu Ala Val Tyr Glu Ala Ile Phe Gly Lys Pro Lys Glu
        275                 280                 285

Lys Val Tyr Ala His Glu Ile Ala Glu Ala Trp Glu Thr Gly Lys Gly
    290                 295                 300

Leu Glu Arg Val Ala Lys Tyr Ser Met Glu Asp Ala Lys Val Thr Tyr
305                 310                 315                 320

Glu Leu Gly Arg Glu Phe Phe Pro Met Glu Ala Gln Leu Ser Arg Leu
            325                 330                 335

Val Gly Gln Pro Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu
            340                 345                 350

Val Glu Trp Tyr Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Leu Ala
            355                 360                 365

Pro Asn Lys Pro Asp Glu Arg Glu Tyr Glu Arg Arg Leu Arg Glu Ser
    370                 375                 380

Tyr Ala Gly Gly Tyr Val Lys Glu Pro Glu Lys Gly Leu Trp Glu Gly
385                 390                 395                 400

Leu Val Ser Leu Asp Phe Arg Ser Leu Tyr Pro Ser Ile Ile Ile Thr
            405                 410                 415

His Asn Val Ser Pro Asp Thr Leu Asn Arg Glu Gly Cys Arg Glu Tyr
            420                 425                 430

Asp Val Ala Pro Glu Val Gly His Lys Phe Cys Lys Asp Phe Pro Gly
        435                 440                 445

Phe Ile Pro Ser Leu Leu Lys Arg Leu Leu Asp Glu Arg Gln Glu Ile
    450                 455                 460

Lys Arg Lys Met Lys Ala Ser Lys Asp Pro Ile Glu Lys Lys Met Leu
465                 470                 475                 480

Asp Tyr Arg Gln Arg Ala Ile Lys Ile Leu Ala Asn Ser
            485                 490
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<210> 4
<211> 283
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:BlastP
     alignment Pyrococcus sp. GB-D DNA polymerase (Deep
     Vent) subject sequence

<400> 4
Asn Ser Tyr Tyr Gly Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys
 1   5   10   15

Lys Glu Cys Ala Glu Ser Val Thr Ala Trp Gly Arg Glu Tyr Ile Glu
            20   25   30

Phe Val Arg Lys Glu Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr
            35   40   45

Ile Asp Thr Asp Gly Leu Tyr Ala Thr Ile Pro Gly Ala Lys Pro Glu
    50   55   60

Glu Ile Lys Lys Lys Ala Leu Glu Phe Val Asp Tyr Ile Asn Ala Lys
 65   70   75   80

Leu Pro Gly Leu Leu Glu Leu Glu Tyr Glu Gly Phe Tyr Val Arg Gly
                85   90   95

Phe Phe Val Thr Lys Lys Lys Tyr Ala Leu Ile Asp Glu Glu Gly Lys
            100   105   110

Ile Ile Thr Arg Gly Leu Glu Ile Val Arg Arg Asp Trp Ser Glu Ile
        115   120   125

Ala Lys Glu Thr Gln Ala Lys Val Leu Glu Ala Ile Leu Lys His Gly
    130   135   140

Asn Val Glu Glu Ala Val Lys Ile Val Lys Glu Val Thr Glu Lys Leu
145   150   155   160

Ser Lys Tyr Glu Ile Pro Pro Glu Lys Leu Val Ile Tyr Glu Gln Ile
                165   170   175

Thr Arg Pro Leu His Glu Tyr Lys Ala Ile Gly Pro His Val Ala Val
            180   185   190

Ala Lys Arg Leu Ala Ala Arg Gly Val Lys Val Arg Pro Gly Met Val
            195   200   205

Ile Gly Tyr Ile Val Leu Arg Gly Asp Gly Pro Ile Ser Lys Arg Ala
    210   215   220

Ile Leu Ala Glu Glu Phe Asp Leu Arg Lys His Lys Tyr Asp Ala Glu
225   230   235   240

Tyr Tyr Ile Glu Asn Gln Val Leu Pro Ala Val Leu Arg Ile Leu Glu
            245   250   255

6

Ala Phe Gly Tyr Arg Lys Glu Asp Leu Arg Trp Gln Lys Thr Lys Gln
            260   265   270

Thr Gly Leu Thr Ala Trp Leu Asn Ile Lys Lys
        275   280

<210> 5
<211> 493
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:BlastP
      alignment consensus sequence

<220>
<221> MOD_RES
<222> (1)..(493)
<223> Xaa = unknown amino acid

<400> 5
Met Ile Leu Asp Xaa Asp Tyr Ile Thr Glu Xaa Gly Lys Pro Xaa Ile
  1   5   10   15

Arg Xaa Phe Lys Lys Glu Asn Gly Xaa Phe Lys Xaa Glu Xaa Asp Arg
            20   25   30

Xaa Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Xaa Asp Asp Ser Xaa Ile
        35   40   45

Xaa Glu Val Xaa Lys Ile Thr Xaa Glu Arg His Gly Lys Ile Val Arg
    50   55   60

Ile Xaa Asp Xaa Glu Lys Val Xaa Lys Lys Phe Leu Gly Xaa Pro Ile
 65   70   75   80

Xaa Val Trp Xaa Leu Tyr Xaa Glu His Pro Gln Asp Val Pro Xaa Ile
            85   90   95

Arg Xaa Lys Xaa Arg Glu His Xaa Ala Val Xaa Asp Ile Phe Glu Tyr
        100   105   110

Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro
        115   120   125

Met Glu Gly Xaa Glu Glu Leu Lys Xaa Leu Ala Phe Asp Ile Glu Thr
    130   135   140

Leu Tyr His Glu Gly Glu Glu Phe Xaa Lys Gly Pro Ile Ile Met Ile
145   150   155   160

Ser Tyr Ala Asp Glu Xaa Glu Ala Lys Val Ile Thr Trp Lys Xaa Ile
                165   170   175

Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile Lys
            180   185   190

Arg Phe Leu Xaa Xaa Ile Arg Glu Lys Asp Pro Asp Xaa Ile Xaa Thr
        195   200   205

7

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Tyr Asn Gly Asp Ser Phe Asp Xaa Pro Tyr Leu Xaa Lys Arg Ala Glu
    210                 215                 220

Lys Leu Gly Ile Lys Leu Xaa Xaa Gly Arg Asp Gly Ser Glu Pro Lys
225                 230                 235                 240

Met Gln Arg Xaa Gly Asp Met Thr Ala Val Glu Xaa Lys Gly Arg Ile
            245                 250                 255

His Phe Asp Leu Tyr His Val Ile Xaa Arg Thr Ile Asn Leu Pro Thr
            260                 265                 270

Tyr Thr Leu Glu Ala Val Tyr Glu Ala Ile Phe Gly Lys Pro Lys Glu
            275                 280                 285

Lys Val Tyr Ala Xaa Glu Ile Ala Xaa Ala Trp Glu Xaa Gly Xaa Xaa
    290                 295                 300

Leu Glu Arg Val Ala Lys Tyr Ser Met Glu Asp Ala Lys Xaa Thr Tyr
305                 310                 315                 320

Glu Leu Gly Xaa Glu Phe Xaa Pro Met Glu Xaa Gln Leu Ser Arg Leu
            325                 330                 335

Val Gly Gln Pro Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu
            340                 345                 350

Val Glu Trp Xaa Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Xaa Ala
            355                 360                 365

Pro Asn Lys Pro Xaa Glu Xaa Glu Tyr Xaa Arg Arg Leu Arg Glu Ser
    370                 375                 380

Tyr Xaa Gly Gly Xaa Val Lys Glu Pro Glu Lys Gly Leu Trp Glu Xaa
385                 390                 395                 400

Xaa Val Xaa Leu Asp Phe Arg Xaa Leu Tyr Pro Ser Ile Ile Ile Thr
            405                 410                 415

His Asn Val Ser Pro Asp Thr Leu Asn Xaa Glu Gly Cys Xaa Xaa Tyr
            420                 425                 430

Asp Xaa Ala Pro Xaa Val Gly His Lys Phe Cys Lys Asp Xaa Pro Gly
    435                 440                 445

Phe Ile Pro Ser Leu Leu Xaa Xaa Leu Leu Xaa Glu Arg Gln Xaa Ile
    450                 455                 460

Lys Xaa Lys Met Lys Xaa Xaa Xaa Asp Pro Ile Glu Lys Xaa Xaa Leu
465                 470                 475                 480

Asp Tyr Arg Gln Xaa Ala Ile Lys Xaa Leu Ala Asn Ser
            485                 490
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<210> 6
<211> 283
<212> PRT
<213> Artificial Sequence

8

<220>
<223> Description of Artificial Sequence:BlastP
      alignment consensus sequence

<220>
<221> MOD_RES
<222> (1)..(283)
<223> Xaa = unknown amino acid

<400> 6
Asn Ser Xaa Tyr Gly Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys
  1   5   10   15

Lys Glu Cys Ala Glu Ser Val Thr Ala Trp Gly Arg Xaa Tyr Ile Glu
             20   25   30

Xaa Val Xaa Lys Glu Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr
         35   40   45

Ile Asp Thr Asp Gly Leu Tyr Ala Thr Ile Pro Gly Xaa Xaa Xaa Glu
     50   55   60

Glu Ile Lys Lys Lys Ala Leu Glu Phe Val Xaa Tyr Ile Asn Xaa Lys
 65   70   75   80

Leu Pro Gly Leu Leu Glu Leu Glu Tyr Glu Gly Phe Tyr Xaa Arg Gly
                 85   90   95

Phe Phe Val Thr Lys Lys Xaa Tyr Ala Xaa Ile Asp Glu Glu Gly Lys
             100   105   110

Xaa Ile Thr Arg Gly Leu Glu Ile Val Arg Arg Asp Trp Ser Glu Ile
         115   120   125

Ala Lys Glu Thr Gln Ala Xaa Val Leu Glu Xaa Ile Leu Lys His Gly
     130   135   140

Xaa Val Glu Glu Ala Val Xaa Ile Val Lys Glu Val Xaa Xaa Lys Leu
145   150   155   160

Xaa Xaa Tyr Glu Ile Pro Pro Glu Lys Leu Xaa Ile Tyr Glu Gln Ile
             165   170   175

Thr Arg Pro Leu His Glu Tyr Lys Ala Ile Gly Pro His Val Ala Val
             180   185   190

Ala Lys Xaa Leu Ala Ala Xaa Gly Val Lys Xaa Xaa Pro Gly Met Val
         195   200   205

Ile Gly Tyr Ile Val Leu Arg Gly Asp Gly Pro Ile Ser Xaa Arg Ala
     210   215   220

Ile Leu Ala Glu Glu Xaa Asp Xaa Xaa Lys His Lys Tyr Asp Ala Glu
225   230   235   240

Tyr Tyr Ile Glu Asn Gln Val Leu Pro Ala Val Leu Arg Ile Leu Glu
             245   250   255

Xaa Phe Gly Tyr Arg Lys Glu Asp Leu Arg Xaa Gln Lys Thr Xaa Gln
            260   265   270

Xaa Gly Leu Thr Xaa Trp Leu Asn Ile Lys Lys
        275   280

<210> 7
<211> 151
<212> PRT
<213> Escherichia coli

<220>
<223> mesophile E. coli deoxyuridine 5'-triphosphate
      nucleotidohydrolase (dUTPase or Dut) (ECD)

<400> 7
Met Lys Lys Ile Asp Val Lys Ile Leu Asp Pro Arg Val Gly Lys Glu
  1   5   10   15

Phe Pro Leu Pro Thr Tyr Ala Thr Ser Gly Ser Ala Gly Leu Asp Leu
            20   25   30

Arg Ala Cys Leu Asn Asp Ala Val Glu Leu Ala Pro Gly Asp Thr Thr
        35   40   45

Leu Val Pro Thr Gly Leu Ala Ile His Ile Ala Asp Pro Ser Leu Ala
     50   55   60

Ala Met Met Leu Pro Arg Ser Gly Leu Gly His Lys His Gly Ile Val
 65   70   75   80

Leu Gly Asn Leu Val Gly Leu Ile Asp Ser Asp Tyr Gln Gly Gln Leu
            85   90   95

Met Ile Ser Val Trp Asn Arg Gly Gln Asp Ser Phe Thr Ile Gln Pro
            100   105   110

Gly Glu Arg Ile Ala Gln Met Ile Phe Val Pro Val Val Gln Ala Glu
        115   120   125

Phe Asn Leu Val Glu Asp Phe Asp Ala Thr Asp Arg Gly Glu Gly Gly
    130   135   140

Phe Gly His Ser Gly Arg Gln
145   150

<210> 8
<211> 150
<212> PRT
<213> Aquifex aeolicus

<220>
<223> deoxyuridine 5'-triphosphate nucleotidohydrolase
      (dUTPase or Dut) (AAD)

<400> 8
Met Ser Lys Val Ile Leu Lys Ile Lys Arg Leu Pro His Ala Gln Asp
  1   5   10   15

10

Leu Pro Leu Pro Ser Tyr Ala Thr Pro His Ser Ser Gly Leu Asp Leu
            20   25   30

Arg Ala Ala Ile Glu Lys Pro Leu Lys Ile Lys Pro Phe Glu Arg Val
        35   40   45

Leu Ile Pro Thr Gly Leu Ile Leu Glu Ile Pro Glu Gly Tyr Glu Gly
    50   55   60

Gln Val Arg Pro Arg Ser Gly Leu Ala Trp Lys Lys Gly Leu Thr Val
65   70   75   80

Leu Asn Ala Pro Gly Thr Ile Asp Ala Asp Tyr Arg Gly Glu Val Lys
                85   90   95

Val Ile Leu Val Asn Leu Gly Asn Glu Glu Val Val Ile Glu Arg Gly
            100   105   110

Glu Arg Ile Ala Gln Leu Val Ile Ala Pro Val Gln Arg Val Glu Val
        115   120   125

Val Glu Val Glu Glu Val Ser Gln Thr Gln Arg Gly Glu Gly Gly Phe
    130   135   140

Gly Ser Thr Gly Thr Lys
145   150

<210> 9
<211> 149
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:E. coli
      deoxyuridine 5'-triphosphate nucleotidohydrolase
      (dUTPase or Dut) (ECD) BlastP alignment sequence

<400> 9
Met Lys Lys Ile Asp Val Lys Ile Leu Asp Pro Arg Val Gly Lys Glu
  1   5   10   15

Phe Pro Leu Pro Thr Tyr Ala Thr Ser Gly Ser Ala Gly Leu Asp Leu
            20   25   30

Arg Ala Cys Leu Asn Asp Ala Val Glu Leu Ala Pro Gly Asp Thr Thr
        35   40   45

Leu Val Pro Thr Gly Leu Ala Ile His Ile Ala Asp Pro Ser Leu Ala
    50   55   60

Ala Met Met Leu Pro Arg Ser Gly Leu Gly His Lys His Gly Ile Val
65   70   75   80

Leu Gly Asn Leu Val Gly Leu Ile Asp Ser Asp Tyr Gln Gly Gln Leu
                85   90   95

Met Ile Ser Val Trp Asn Arg Gly Gln Asp Ser Phe Thr Ile Gln Pro
            100   105   110

Gly Glu Arg Ile Ala Gln Met Ile Phe Val Pro Val Val Gln Ala Glu
        115   120   125

Phe Asn Leu Val Glu Asp Phe Asp Ala Thr Asp Arg Gly Glu Gly Gly
    130   135   140

Phe Gly His Ser Gly
145

<210> 10
<211> 148
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Aquifex
     aeolicus deoxyuridine 5'-triphosphate
     nucleotidohydrolase (dUTPase or Dut) (AAD) BlastP
     alignment sequence

<400> 10
Met Ser Lys Val Ile Leu Lys Ile Lys Arg Leu Pro His Ala Gln Asp
  1   5   10   15

Leu Pro Leu Pro Ser Tyr Ala Thr Pro His Ser Ser Gly Leu Asp Leu
            20   25   30

Arg Ala Ala Ile Glu Lys Pro Leu Lys Ile Lys Pro Phe Glu Arg Val
        35   40   45

Leu Ile Pro Thr Gly Leu Ile Leu Glu Ile Pro Glu Gly Tyr Glu Gly
    50   55   60

Gln Val Arg Pro Arg Ser Gly Leu Ala Trp Lys Lys Gly Leu Thr Val
65   70   75   80

Leu Asn Ala Pro Gly Thr Ile Asp Ala Asp Tyr Arg Gly Glu Val Lys
            85   90   95

Val Ile Leu Val Asn Leu Gly Asn Glu Glu Val Val Ile Glu Arg Gly
            100   105   110

Glu Arg Ile Ala Gln Leu Val Ile Ala Pro Val Gln Arg Val Glu Val
        115   120   125

Val Glu Val Glu Glu Val Ser Gln Thr Gln Arg Gly Glu Gly Gly Phe
    130   135   140

Gly Ser Thr Gly
145

<210> 11
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus
     sequence

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<400> 11
Gly Leu Asp Leu Arg Ala
  1               5


<210> 12
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus
      sequence

<400> 12
Pro Thr Gly Leu
  1


<210> 13
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus
      sequence

<400> 13
Pro Arg Ser Gly Leu
  1               5


<210> 14
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus
      sequence

<400> 14
Gly Glu Arg Ile Ala Gln
  1               5


<210> 15
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus
      sequence

<400> 15
Arg Gly Glu Gly Gly Phe Gly
  1               5
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<210> 16
<211> 459
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus
     sequence, minimal encoding sequence using
     preferred E. coli codons

<400> 16
atgarmaaar ttrwtstgaa aattmwgsrt cygcstswtg scmaagawtt wccgctgccg 60
asctatgcga ccyctsrcag ckcaggcctg gatctgcgtg cgkscmttra saawscgstg 120
raamttrmgc cgkktgawas grygctgrtt ccgaccggcc tgrycmttsa wattscggaw 180
ssttmtctgg mggsgmwgrt gckgccgcgt agcggcctgg scyrkaaama kggcwtaryg 240
stgskgaacs ygsygggcmy gattgatrsc gattatcrgg gcsaastgaw grttakcstg 300
kkgaacckgg gcmasgawkm akttrygatt sagcsgggcg aacgtattgc gcagmtgrtt 360
wttgygccgg tgswgcrggy ggaakttrwt swggtggaag awkttkmtsm gaccsakcgt 420
ggcgaaggcg gctttggcym tascggcasa magtaatga 459

<210> 17
<211> 151
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus
     sequence, minimal encoding sequence translation

<220>
<221> MOD_RES
<222> (2)
<223> Xaa = Lys, Ser, Arg or Asn

<220>
<221> MOD_RES
<222> (4)
<223> Xaa = Ile or Val

<220>
<221> MOD_RES
<222> (5)
<223> Xaa = Asp, Ile, Val or Asn

<220>
<221> MOD_RES
<222> (6)
<223> Xaa = Val or Leu

<220>
<221> MOD_RES
<222> (9)
<223> Xaa = Leu, Lys, Gln or Met

<220>
<221> MOD_RES
<222> (10)
<223> Xaa = Asp, Arg, Gly or His

14

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<220>
<221> MOD_RES
<222> (11)
<223> Xaa = Pro or Leu

<220>
<221> MOD_RES
<222> (12)
<223> Xaa = Arg or Pro

<220>
<221> MOD_RES
<222> (13)
<223> Xaa = Val, His, Asp or Leu

<220>
<221> MOD_RES
<222> (14)
<223> Xaa = Gly or Ala

<220>
<221> MOD_RES
<222> (15)
<223> Xaa = Lys or Gln

<220>
<221> MOD_RES
<222> (16)
<223> Xaa = Glu or Asp

<220>
<221> MOD_RES
<222> (17)
<223> Xaa = Phe or Leu

<220>
<221> MOD_RES
<222> (21)
<223> Xaa = Thr or Ser

<220>
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<222> (25)
<223> Xaa = Ser or Pro

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<221> MOD_RES
<222> (26)
<223> Xaa = Gly, His, Asp or Arg

<220>
<221> MOD_RES
<222> (28)
<223> Xaa = Ala or Ser

<220>
<221> MOD_RES
<222> (35)
<223> Xaa = Cys, Ala, Ser or Gly
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<220>
<221> MOD_RES
<222> (36)
<223> Xaa = Leu or Ile

<220>
<221> MOD_RES
<222> (37)
<223> Xaa = Asn, Glu, Lys or Asp

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Xaa Pro Leu Pro Xaa Tyr Ala Thr Xaa Xaa Ser Xaa Gly Leu Asp Leu
              20                  25                  30

Arg Ala Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Pro Xaa Xaa Xaa Xaa
          35                  40                  45

Leu Xaa Pro Thr Gly Leu Xaa Xaa Xaa Ile Xaa Xaa Xaa Xaa Leu Xaa
    50                  55                  60

Xaa Xaa Xaa Xaa Pro Arg Ser Gly Leu Xaa Xaa Lys Xaa Gly Xaa Xaa
  65                  70                  75                  80
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21

```
Xaa Xaa Asn Xaa Xaa Gly Xaa Ile Asp Xaa Asp Tyr Xaa Gly Glx Xaa
                85                  90              95

Xaa Xaa Xaa Xaa Xaa Asn Xaa Gly Xaa Xaa Xaa Xaa Xaa Ile Glx Xaa
            100             105             110

Gly Glu Arg Ile Ala Gln Xaa Xaa Xaa Xaa Pro Val Xaa Xaa Xaa Glu
        115                 120             125

Xaa Xaa Xaa Val Glu Xaa Xaa Xaa Xaa Thr Xaa Arg Gly Glu Gly Gly
    130             135             140

Phe Gly Xaa Xaa Gly Xaa Xaa
145                 150
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<210> 18
<211> 456
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus
      sequence, minimal encoding sequence after removal
      of non-similar degeneracies and selection of AAD
      parent residues

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asctatgcga ccyctcacag ckcaggcctg gatctgcgtg cgkscmttra saawscgstg 120
raamttrmgc cgkktgawas grygctgrtt ccgaccggcc tgatcmttsa wattscggaw 180
ggttmtgmgg sgcagrtgck gccgcgtagc ggcctggsct ggaaamakgg cwtarygstg 240
ctgaacgcgs ygggcmygat tgatrscgat tatcrggcs aastgawgrt takcstggtg 300
aacckgggcm asgawgaakt trygattsag csgggcgaac gtattgcgca gmtgrttwtt 360
gygccggtgs wgcrggygga akttrwtswg gtggaagawk tttctcagac csakcgtggc 420
gaaggcggct ttggctctas cggcasamag taatga                          456
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<210> 19
<211> 150
<212> PRT
<213> Artificial Sequence

<220>
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      after removal of non-similar degeneracies and
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<223> Xaa = Asp, Ile, Val or Asn

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<221> MOD_RES
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<223> Xaa = Pro or Leu

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<223> Xaa = Phe or Leu

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<400> 19
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Xaa Pro Leu Pro Xaa Tyr Ala Thr Xaa His Ser Xaa Gly Leu Asp Leu
          20                  25                  30
```

```
Arg Ala Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Pro Xaa Xaa Xaa Xaa
        35                  40                  45

Leu Xaa Pro Thr Gly Leu Ile Xaa Xaa Ile Xaa Xaa Gly Xaa Xaa Xaa
    50                  55                  60

Gln Xaa Xaa Pro Arg Ser Gly Leu Xaa Trp Lys Xaa Gly Xaa Xaa Xaa
65                  70                  75                  80

Leu Asn Ala Xaa Gly Xaa Ile Asp Xaa Asp Tyr Xaa Gly Glx Xaa Xaa
                85                  90      .           95

Xaa Xaa Xaa Asn Asn Xaa Gly Xaa Xaa Glu Xaa Xaa Ile Glx Xaa Gly
            100             105             110

Glu Arg Ile Ala Gln Xaa Xaa Xaa Xaa Pro Val Xaa Xaa Xaa Glu Xaa
        115             120             125

Xaa Xaa Val Glu Xaa Xaa Ser Gln Thr Xaa Arg Gly Glu Gly Gly Phe
    130             135             140

Gly Ser Xaa Gly Xaa Xaa
145                 150


<210> 20
<211> 487
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus
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      of non-similar degeneracies, selection of AAD parent
      residues, priming and restriction sites added to ends
      and codon usage changed to add restriction sites

<400> 20
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aagawttwcc gctgccgasc tatgcgaccy ctcacagckc aggcctggat ctgcgtgcgk 120
scmttrasra wscgstgraa mttrmgccgk ktgawasgry gctgrttccg accggtctga 180
tcmttsawat tscggawggt tmtgmggsgc agrtgckgcc gcgtagcggc ctggsctgga 240
aamakggcwt arygstgctg aacgcgsygg gcmygatcga trscgattat crgggcsaas 300
tgawgrttak cstggtgaac ckgggcmasg awgaakttry gattsagcsg ggcgaacgta 360
ttgcgcagmt grttwttgyg ccggtgswgc rggyggaakt trwtswggtg gaagawkttt 420
ctcagaccsa kcgtggcgaa ggcggctttg gctctascgg casamagtaa tgaggatccg 480
aattctt                                                         487


<210> 21
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<212> PRT
<213> Artificial Sequence

<220>
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      after removal of non-similar degeneracies and
      selection of AAD parent residues
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<223> Xaa = Leu, Lys, Gln or Met

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<223> Xaa = Pro or Leu

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<223> Xaa = Arg or Pro

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<223> Xaa = Arg or Leu

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            20   25   30

Arg Ala Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Pro Xaa Xaa Xaa Xaa
        35   40   45

Leu Xaa Pro Thr Gly Leu Ile Xaa Xaa Ile Xaa Xaa Gly Xaa Xaa Xaa
    50   55   60

Gln Xaa Xaa Pro Arg Ser Gly Leu Xaa Trp Lys Xaa Gly Xaa Xaa Xaa
 65   70   75   80

Leu Asn Ala Xaa Gly Xaa Ile Asp Xaa Asp Tyr Xaa Gly Glx Xaa Xaa
            85   90   95

Xaa Xaa Xaa Asn Asn Xaa Gly Xaa Xaa Glu Xaa Xaa Ile Glx Xaa Gly
        100   105   110

Glu Arg Ile Ala Gln Xaa Xaa Xaa Xaa Pro Val Xaa Xaa Xaa Glu Xaa
    115   120   125

Xaa Xaa Val Glu Xaa Xaa Ser Gln Thr Xaa Arg Gly Glu Gly Gly Phe
    130   135   140

Gly Ser Xaa Gly Xaa Xaa
145   150

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      hybrid DNA polymerase minimal encoding sequence

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ctgctgarag atgattctma gattgakgaa gttaraaaaa tcactgstga gcgccatggc 180
aagattgttc gtatcrttga tgyggaaaag gtarrgaaga aatttctggg caraccaatc 240
rmggtgtgga ractgtatyt cgaacatcca caagatgttc cgaytattcg cgakaaartt 300
cgcgaacaty ctgcagttrt tgacatcttc gaatacgata ttccatttgc aaagcgttac 360
ctcatcgaca aaggcctgat accaatggag ggcgakgaag aactcaagmt cctggcgttc 420
gatatagaaa ccctctatca cgaaggcgaa gagtttgsta aaggcccaat tataatgatt 480
agctatgcag atgaaaramga agcaaaggtg attacttgga aaaamataga tctcccatac 540
gttgaggttg tatcttccga gcgcgagatg attaagcgct ttctcararrt tatccgcgag 600
aaggatccgg acrttatcrt tacttataac ggcgactctt ttgacytccc atatctggyg 660
aaacgcgcag aaaaactcgg tattaaactg mctmtcggcc gtgatggttc cgagccgaag 720
atgcagcgtm tcggcgatat gaccgctgta gaarttaagg gtcgtatcca tttcgacctg 780
tatcatgtaa ttmsccgtac tattaacctc ccgacttaca ctctcgaggc tgtatatgaa 840

36

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gcaattttttg gtaagccgaa ggagaaggta tacgccsatg agattgcara ggcgtgggaa 900
wccggtragr rcctcgagcg tgttgcaaaa tactccatgg aagatgcaaa ggygacttat 960
gaactcggca ragaattcyt cccaatggaa rytcagctct ctcgcctggt tggccaacca 1020
ctgtgggatg tttctcgttc ttccaccggt aacctcgtag agtggtwtct cctgcgcaaa 1080
gcgtacgaac gcaacgaast ggctccgaac aagccakmcg aasragagta tsaacgccgt 1140
ctccgcgagt cttacrctgg tggctwtgtt aaagagccag aaaagggcct ctgggaarrc 1200
mtcgtgtmcc tcgattttcg ckctctgtat ccgtctatta tcattaccca caacgtgtct 1260
ccggatactc tcaacckcga gggctgcara ramtatgatr ttgctccgsa agtaggccac 1320
aagttctgca aggacwtccc gggctttatt ccgtctctcc tgrrgcrtct gctcgakgaa 1380
cgccaaraga ttaagmscaa aatgaaggmg wccmaggatc cgattgaaaa aawamtgctc 1440
gactatcgcc aaaragcgat taaamtcctc gcaaactctt wttacggcta ttatggctat 1500
gcaaaagcac gctggtactg taaggagtgt gctgagtccg ttactgcttg gggtcgcraa 1560
tacatcgagy tcgtgcyggaa ggagctcgaa gaaaagtttg gctttaaagt tctctacatt 1620
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ctcgygattt atgagcagat tactcgcccg ctgcatgagt ataaggcgat tggtccgcac 2040
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gcggtactcc gtattctgga ggsttttggc taccgtaagg aagacctccg ctrscaaaag 2280
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tagcatgac                                                      2349


<210> 23
<211> 778
<212> PRT
<213> Artificial Sequence

<220>
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      hybrid DNA polymerase minimal encoding sequence
      translation

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            20   25   30

Xaa Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Xaa Asp Asp Ser Xaa Ile
            35   40   45

Xaa Glu Val Xaa Lys Ile Thr Xaa Glu Arg His Gly Lys Ile Val Arg
    50   55   60

Ile Xaa Asp Xaa Glu Lys Val Xaa Lys Lys Phe Leu Gly Xaa Pro Ile
65   70   75   80

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Xaa Val Trp Xaa Leu Tyr Xaa Glu His Pro Gln Asp Val Pro Xaa Ile
             85                  90                    95

Arg Xaa Lys Xaa Arg Glu His Xaa Ala Val Xaa Asp Ile Phe Glu Tyr
        100              105              110

Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro
        115              120              125

Met Glu Gly Xaa Glu Glu Leu Lys Xaa Leu Ala Phe Asp Ile Glu Thr
130              135              140

Leu Tyr His Glu Gly Glu·Glu Phe Xaa Lys Gly Pro Ile Ile Met Ile
145              150              155                  160

Ser Tyr Ala Asp Glu Xaa Glu Ala Lys Val Ile Thr Trp Lys Xaa Ile
             165              170              175

Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile Lys
             180                  185              190

Arg Phe Leu Xaa Xaa Ile Arg Glu Lys Asp Pro Asp Xaa Ile Xaa Thr
        195              200              205

Tyr Asn Gly Asp Ser Phe Asp Xaa Pro Tyr Leu Xaa Lys Arg Ala Glu
    210              215              220

Lys Leu Gly Ile Lys Leu Xaa Xaa Gly Arg Asp Gly Ser Glu Pro Lys
225              230              235                  240

Met Gln Arg Xaa Gly Asp Met Thr Ala Val Glu Xaa Lys Gly Arg Ile
        245              250              255

His Phe Asp Leu Tyr His Val Ile Xaa Arg Thr Ile Asn Leu Pro Thr
        260              265              270

Tyr Thr Leu Glu Ala Val Tyr Glu Ala Ile Phe Gly Lys Pro Lys Glu
        275              280              285

Lys Val Tyr Ala Xaa Glu Ile Ala Xaa Ala Trp Glu Xaa Gly Xaa Xaa
    290              295              300

Leu Glu Arg Val Ala Lys Tyr Ser Met Glu Asp Ala Lys Xaa Thr Tyr
305              310              315                  320

Glu Leu Gly Xaa Glu Phe Xaa Pro Met Glu Xaa Gln Leu Ser Arg Leu
             325              330              335

Val Gly Gln Pro Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu
             340              345              350

Val Glu Trp Xaa Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Xaa Ala
        355              360              365

Pro Asn Lys Pro Xaa Glu Xaa Glu Tyr Glx Arg Arg Leu Arg Glu Ser
    370              375              380

Tyr Xaa Gly Gly Xaa Val Lys Glu Pro Glu Lys Gly Leu Trp Glu Xaa
385              390              395                  400
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Xaa Val Xaa Leu Asp Phe Arg Xaa Leu Tyr Pro Ser Ile Ile Ile Thr
            405   410   415

His Asn Val Ser Pro Asp Thr Leu Asn Xaa Glu Gly Cys Xaa Xaa Tyr
            420   425   430

Asp Xaa Ala Pro Glx Val Gly His Lys Phe Cys Lys Asp Xaa Pro Gly
        435   440   445

Phe Ile Pro Ser Leu Leu Xaa Xaa Leu Leu Xaa Glu Arg Gln Xaa Ile
    450   455   460

Lys Xaa Lys Met Lys Xaa Xaa Xaa Asp Pro Ile Glu Lys Xaa Xaa Leu
465   470   475   480

Asp Tyr Arg Gln Xaa Ala Ile Lys Xaa Leu Ala Asn Ser Xaa Tyr Gly
            485   490   495

Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu
        500   505   510

Ser Val Thr Ala Trp Gly Arg Xaa Tyr Ile Glu Xaa Val Xaa Lys Glu
        515   520   525

Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ile Asp Thr Asp Gly
    530   535   540

Leu Tyr Ala Thr Ile Pro Gly Xaa Xaa Xaa Glu Glu Ile Lys Lys Lys
545   550   555   560

Ala Leu Glu Phe Val Lys Tyr Ile Asn Xaa Lys Leu Pro Gly Leu Leu
            565   570   575

Glu Leu Glu Tyr Glu Gly Phe Tyr Xaa Arg Gly Phe Phe Val Thr Lys
        580   585   590

Lys Xaa Tyr Ala Xaa Ile Asp Glu Glu Gly Lys Xaa Ile Thr Arg Gly
        595   600   605

Leu Glu Ile Val Arg Arg Asp Trp Ser Glu Ile Ala Lys Glu Thr Gln
    610   615   620

Ala Xaa Val Leu Glu Xaa Ile Leu Lys His Gly Asx Val Glu Glu Ala
625   630   635   640

Val Xaa Ile Val Lys Glu Val Xaa Glx Lys Leu Xaa Xaa Tyr Glu Ile
            645   650   655

Pro Pro Glu Lys Leu Xaa Ile Tyr Glu Gln Ile Thr Arg Pro Leu His
        660   665   670

Glu Tyr Lys Ala Ile Gly Pro His Val Ala Val Ala Lys Xaa Leu Ala
        675   680   685

Ala Xaa Gly Val Lys Xaa Xaa Pro Gly Met Val Ile Gly Tyr Ile Val
    690   695   700

Leu Arg Gly Asp Gly Pro Ile Ser Xaa Arg Ala Ile Leu Ala Glu Glu
705   710   715   720

48

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Gln Val Leu Pro Ala Val Leu Arg Ile Leu Glu Xaa Phe Gly Tyr Arg
              740                 745                 750

Lys Glu Asp Leu Arg Xaa Gln Lys Thr Xaa Gln Xaa Gly Leu Thr Xaa
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Trp Leu Asn Ile Lys Lys Ser Gly Thr His
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<212> PRT
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<220>
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      Pyrococcus furiosus family B DNA polymerase (Pfu)

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Arg Leu Phe Lys Lys Glu Asn Gly Lys Phe Lys Ile Glu His Asp Arg
              20                  25                  30

Thr Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Arg Asp Asp Ser Lys Ile
          35                  40                  45

Glu Glu Val Lys Lys Ile Thr Gly Glu Arg His Gly Lys Ile Val Arg
      50                  55                  60

Ile Val Asp Val Glu Lys Val Glu Lys Lys Phe Leu Gly Lys Pro Ile
 65                  70                  75                  80

Thr Val Trp Lys Leu Tyr Leu Glu His Pro Gln Asp Val Pro Thr Ile
              85                  90                  95

Arg Glu Lys Val Arg Glu His Pro Ala Val Val Asp Ile Phe Glu Tyr
              100                 105                 110

Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro
          115                 120                 125

Met Glu Gly Glu Glu Glu Leu Lys Ile Leu Ala Phe Asp Ile Glu Thr
      130                 135                 140

Leu Tyr His Glu Gly Glu Glu Phe Gly Lys Gly Pro Ile Ile Met Ile
145                 150                 155                 160

Ser Tyr Ala Asp Glu Asn Glu Ala Lys Val Ile Thr Trp Lys Asn Ile
              165                 170                 175

Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile Lys
              180                 185                 190

Arg Phe Leu Arg Ile Ile Arg Glu Lys Asp Pro Asp Ile Ile Val Thr
          195                 200                 205
```

49

```
Tyr Asn Gly Asp Ser Phe Asp Phe Pro Tyr Leu Ala Lys Arg Ala Glu
    210             215             220

Lys Leu Gly Ile Lys Leu Thr Ile Gly Arg Asp Gly Ser Glu Pro Lys
225             230             235             240

Met Gln Arg Ile Gly Asp Met Thr Ala Val Glu Val Lys Gly Arg Ile
            245             250             255

His Phe Asp Leu Tyr His Val Ile Thr Arg Thr Ile Asn Leu Pro Thr
            260             265             270

Tyr Thr Leu Glu Ala Val Tyr Glu Ala Ile Phe Gly Lys Pro Lys Glu
            275             280             285

Lys Val Tyr Ala Asp Glu Ile Ala Lys Ala Trp Glu Ser Gly Glu Asn
    290             295             300

Leu Glu Arg Val Ala Lys Tyr Ser Met Glu Asp Ala Lys Ala Thr Tyr
305             310             315             320

Glu Leu Gly Lys Glu Phe Leu Pro Met Glu Ile Gln Leu Ser Arg Leu
            325             330             335

Val Gly Gln Pro Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu
            340             345             350

Val Glu Trp Phe Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Val Ala
            355             360             365

Pro Asn Lys Pro Ser Glu Glu Glu Tyr Gln Arg Arg Leu Arg Glu Ser
    370             375             380

Tyr Thr Gly Gly Phe Val Lys Glu Pro Glu Lys Gly Leu Trp Glu Asn
385             390             395             400

Ile Val Tyr Leu Asp Phe Arg Ala Leu Tyr Pro Ser Ile Ile Ile Thr
            405             410             415

His Asn Val Ser Pro Asp Thr Leu Asn Leu Glu Gly Cys Lys Asn Tyr
            420             425             430

Asp Ile Ala Pro Gln Val Gly His Lys Phe Cys Lys Asp Ile Pro Gly
            435             440             445

Phe Ile Pro Ser Leu Leu Gly His Leu Leu Glu Glu Arg Gln Lys Ile
    450             455             460

Lys Thr Lys Met Lys Glu Thr Gln Asp Pro Ile Glu Lys Ile Leu Leu
465             470             475             480

Asp Tyr Arg Gln Lys Ala Ile Lys Leu Leu Ala Asn Ser Phe Tyr Gly
            485             490             495

Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu
            500             505             510

Ser Val Thr Ala Trp Gly Arg Lys Tyr Ile Glu Leu Val Trp Lys Glu
            515             520             525
```

```
Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ile Asp Thr Asp Gly
    530             535             540
Leu Tyr Ala Thr Ile Pro Gly Gly Glu Ser Glu Glu Ile Lys Lys Lys
545             550             555             560
Ala Leu Glu Phe Val Lys Tyr Ile Asn Ser Lys Leu Pro Gly Leu Leu
            565             570             575
Glu Leu Glu Tyr Glu Gly Phe Tyr Lys Arg Gly Phe Phe Val Thr Lys
            580             585             590
Lys Arg Tyr Ala Val Ile Asp Glu Glu Gly Lys Val Ile Thr Arg Gly
        595             600             605
Leu Glu Ile Val Arg Arg Asp Trp Ser Glu Ile Ala Lys Glu Thr Gln
    610             615             620
Ala Arg Val Leu Glu Thr Ile Leu Lys His Gly Asp Val Glu Glu Ala
625             630             635             640
Val Arg Ile Val Lys Glu Val Ile Gln Lys Leu Ala Asn Tyr Glu Ile
            645             650             655
Pro Pro Glu Lys Leu Ala Ile Tyr Glu Gln Ile Thr Arg Pro Leu His
            660             665             670
Glu Tyr Lys Ala Ile Gly Pro His Val Ala Val Ala Lys Lys Leu Ala
        675             680             685
Ala Lys Gly Val Lys Ile Lys Pro Gly Met Val Ile Gly Tyr Ile Val
    690             695             700
Leu Arg Gly Asp Gly Pro Ile Ser Asn Arg Ala Ile Leu Ala Glu Glu
705             710             715             720
Tyr Asp Pro Lys Lys His Lys Tyr Asp Ala Glu Tyr Tyr Ile Glu Asn
            725             730             735
Gln Val Leu Pro Ala Val Leu Arg Ile Leu Glu Gly Phe Gly Tyr Arg
            740             745             750
Lys Glu Asp Leu Arg Tyr Gln Lys Thr Arg Gln Val Gly Leu Thr Ser
            755             760             765
Trp Leu Asn Ile Lys Lys Ser
    770             775


<210> 25
<211> 775
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:parent
      Pyrococcus sp. GD-B (Deep Vent) DNA polymerase

<400> 25
Met Ile Leu Asp Ala Asp Tyr Ile Thr Glu Asp Gly Lys Pro Ile Ile
  1           5               10              15
```

Arg Ile Phe Lys Lys Glu Asn Gly Glu Phe Lys Val Glu Tyr Asp Arg
              20   25   30

Asn Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Lys Asp Asp Ser Gln Ile
              35   40   45

Asp Glu Val Arg Lys Ile Thr Ala Glu Arg His Gly Lys Ile Val Arg
       50   55   60

Ile Ile Asp Ala Glu Lys Val Arg Lys Lys Phe Leu Gly Arg Pro Ile
65   70   75   80

Glu Val Trp Arg Leu Tyr Phe Glu His Pro Gln Asp Val Pro Ala Ile
              85   90   95

Arg Asp Lys Ile Arg Glu His Ser Ala Val Ile Asp Ile Phe Glu Tyr
              100   105   110

Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro
              115   120   125

Met Glu Gly Asp Glu Glu Leu Lys Leu Leu Ala Phe Asp Ile Glu Thr
       130   135   140

Leu Tyr His Glu Gly Glu Glu Phe Ala Lys Gly Pro Ile Ile Met Ile
145   150   155   160

Ser Tyr Ala Asp Glu Glu Glu Ala Lys Val Ile Thr Trp Lys Lys Ile
              165   170   175

Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile Lys
              180   185   190

Arg Phe Leu Lys Val Ile Arg Glu Lys Asp Pro Asp Val Ile Ile Thr
              195   200   205

Tyr Asn Gly Asp Ser Phe Asp Leu Pro Tyr Leu Val Lys Arg Ala Glu
       210   215   220

Lys Leu Gly Ile Lys Leu Pro Leu Gly Arg Asp Gly Ser Glu Pro Lys
225   230   235   240

Met Gln Arg Leu Gly Asp Met Thr Ala Val Glu Ile Lys Gly Arg Ile
              245   250   255

His Phe Asp Leu Tyr His Val Ile Arg Arg Thr Ile Asn Leu Pro Thr
              260   265   270

Tyr Thr Leu Glu Ala Val Tyr Glu Ala Ile Phe Gly Lys Pro Lys Glu
       275   280   285

Lys Val Tyr Ala His Glu Ile Ala Glu Ala Trp Glu Thr Gly Lys Gly
       290   295   300

Leu Glu Arg Val Ala Lys Tyr Ser Met Glu Asp Ala Lys Val Thr Tyr
305   310   315   320

Glu Leu Gly Arg Glu Phe Phe Pro Met Glu Ala Gln Leu Ser Arg Leu
              325   330   335

52

```
Val Gly Gln Pro Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu
            340             345             350

Val Glu Trp Tyr Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Leu Ala
            355             360             365

Pro Asn Lys Pro Asp Glu Arg Glu Tyr Glu Arg Arg Leu Arg Glu Ser
    370             375             380

Tyr Ala Gly Gly Tyr Val Lys Glu Pro Glu Lys Gly Leu Trp Glu Gly
385             390             395             400

Leu Val Ser Leu Asp Phe Arg Ser Leu Tyr Pro Ser Ile Ile Ile Thr
            405             410             415

His Asn Val Ser Pro Asp Thr Leu Asn Arg Glu Gly Cys Arg Glu Tyr
            420             425             430

Asp Val Ala Pro Glu Val Gly His Lys Phe Cys Lys Asp Phe Pro Gly
            435             440             445

Phe Ile Pro Ser Leu Leu Lys Arg Leu Leu Asp Glu Arg Gln Glu Ile
    450             455             460

Lys Arg Lys Met Lys Ala Ser Lys Asp Pro Ile Glu Lys Lys Met Leu
465             470             475             480

Asp Tyr Arg Gln Arg Ala Ile Lys Ile Leu Ala Asn Ser Tyr Tyr Gly
            485             490             495

Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu
            500             505             510

Ser Val Thr Ala Trp Gly Arg Glu Tyr Ile Glu Phe Val Arg Lys Glu
            515             520             525

Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ile Asp Thr Asp Gly
    530             535             540

Leu Tyr Ala Thr Ile Pro Gly Ala Lys Pro Glu Glu Ile Lys Lys Lys
545             550             555             560

Ala Leu Glu Phe Val Asp Tyr Ile Asn Ala Lys Leu Pro Gly Leu Leu
            565             570             575

Glu Leu Glu Tyr Glu Gly Phe Tyr Val Arg Gly Phe Phe Val Thr Lys
            580             585             590

Lys Lys Tyr Ala Leu Ile Asp Glu Glu Gly Lys Ile Ile Thr Arg Gly
            595             600             605

Leu Glu Ile Val Arg Arg Asp Trp Ser Glu Ile Ala Lys Glu Thr Gln
    610             615             620

Ala Lys Val Leu Glu Ala Ile Leu Lys His Gly Asn Val Glu Glu Ala
625             630             635             640

Val Lys Ile Val Lys Glu Val Thr Glu Lys Leu Ser Lys Tyr Glu Ile
            645             650             655
```

53

```
Pro Pro Glu Lys Leu Val Ile Tyr Glu Gln Ile Thr Arg Pro Leu His
            660                 665             670

Glu Tyr Lys Ala Ile Gly Pro His Val Ala Val Ala Lys Arg Leu Ala
            675             680             685

Ala Arg Gly Val Lys Val Arg Pro Gly Met Val Ile Gly Tyr Ile Val
    690                 695             700

Leu Arg Gly Asp Gly Pro Ile Ser Lys Arg Ala Ile Leu Ala Glu Glu
705                 710             715                 720

Phe Asp Leu Arg Lys His Lys Tyr Asp Ala Glu Tyr Tyr Ile Glu Asn
                725             730             735

Gln Val Leu Pro Ala Val Leu Arg Ile Leu Glu Ala Phe Gly Tyr Arg
            740             745             750

Lys Glu Asp Leu Arg Trp Gln Lys Thr Lys Gln Thr Gly Leu Thr Ala
            755             760             765

Trp Leu Asn Ile Lys Lys Lys
    770             775


<210> 26
<211> 783
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:designed hybrid
      polymerase from Figure 11

<220>
<221> MOD_RES
<222> (1)..(783)
<223> Xaa = unknown amino acid

<400> 26
Met Ile Leu Asp Xaa Asp Tyr Ile Thr Glu Xaa Gly Lys Pro Xaa Ile
  1             5                 10                  15

Arg Xaa Phe Lys Lys Glu Asn Gly Xaa Phe Lys Xaa Glu Xaa Asp Arg
            20                  25                  30

Xaa Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Xaa Asp Asp Ser Xaa Ile
            35                  40                  45

Xaa Glu Val Xaa Lys Ile Thr Xaa Glu Arg His Gly Lys Ile Val Arg
    50                  55                  60

Ile Xaa Asp Xaa Glu Lys Val Xaa Lys Lys Phe Leu Gly Xaa Pro Ile
65                  70                  75                  80

Xaa Val Trp Xaa Leu Tyr Xaa Glu His Pro Gln Asp Val Pro Xaa Ile
                85                  90                  95

Arg Xaa Lys Xaa Arg Glu His Xaa Ala Val Xaa Asp Ile Phe Glu Tyr
            100                 105                 110
```

54

```
Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro
        115                 120             125
Met Glu Gly Xaa Glu Glu Leu Lys Xaa Leu Ala Phe Asp Ile Glu Thr
    130             135                 140
Leu Tyr His Glu Gly Glu Glu Phe Xaa Lys Gly Pro Ile Ile Met Ile
145                 150                 155                 160
Ser Tyr Ala Asp Glu Xaa Glu Ala Lys Val Ile Thr Trp Lys Xaa Ile
                165                 170                 175
Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile Lys
                180                 185                 190
Arg Phe Leu Xaa Xaa Ile Arg Glu Lys Asp Pro Asp Xaa Ile Xaa Thr
            195                 200                 205
Tyr Asn Gly Asp Ser Phe Asp Xaa Pro Tyr Leu Xaa Lys Arg Ala Glu
    210                 215                 220
Lys Leu Gly Ile Lys Leu Xaa Xaa Gly Arg Asp Gly Ser Glu Pro Lys
225                 230                 235                 240
Met Gln Arg Xaa Gly Asp Met Thr Ala Val Glu Xaa Lys Gly Arg Ile
            245                 250                 255
His Phe Asp Leu Tyr His Val Ile Xaa Arg Thr Ile Asn Leu Pro Thr
            260                 265                 270
Tyr Thr Leu Glu Ala Val Tyr Glu Ala Ile Phe Gly Lys Pro Lys Glu
            275                 280                 285
Lys Val Tyr Ala Xaa Glu Ile Ala Xaa Ala Trp Glu Xaa Gly Xaa Xaa
    290                 295                 300
Leu Glu Arg Val Ala Lys Tyr Ser Met Glu Asp Ala Lys Xaa Thr Tyr
305                 310                 315                 320
Glu Leu Gly Xaa Glu Phe Xaa Pro Met Glu Xaa Gln Leu Ser Arg Leu
            325                 330                 335
Val Gly Gln Pro Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu
            340                 345                 350
Val Glu Trp Xaa Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Xaa Ala
            355                 360                 365
Pro Asn Lys Pro Xaa Glu Xaa Glu Tyr Xaa Arg Arg Leu Arg Glu Ser
    370                 375                 380
Tyr Xaa Gly Gly Xaa Val Lys Glu Pro Glu Lys Gly Leu Trp Glu Xaa
385                 390                 395                 400
Xaa Val Xaa Leu Asp Phe Arg Xaa Leu Tyr Pro Ser Ile Ile Ile Thr
            405                 410                 415
His Asn Val Ser Pro Asp Thr Leu Asn Xaa Glu Gly Cys Xaa Xaa Tyr
            420                 425                 430
```

55

Asp Xaa Ala Pro Xaa Val Gly His Lys Phe Cys Lys Asp Xaa Pro Gly
        435   440   445

Phe Ile Pro Ser Leu Leu Xaa Xaa Leu Leu Xaa Glu Arg Gln Xaa Ile
    450   455   460

Lys Xaa Lys Met Lys Xaa Xaa Xaa Asp Pro Ile Glu Lys Xaa Xaa Leu
465   470   475   480

Asp Tyr Arg Gln Xaa Ala Ile Lys Xaa Leu Ala Asn Ser Xaa Tyr Gly
                485   490   495

Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu
            500   505   510

Ser Val Thr Ala Trp Gly Arg Xaa Tyr Ile Glu Xaa Val Xaa Lys Glu
        515   520   525

Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ile Asp Thr Asp Gly
    530   535   540

Leu Tyr Ala Thr Ile Pro Gly Xaa Xaa Xaa Glu Glu Ile Lys Lys Lys
545   550   555   560

Ala Leu Glu Phe Val Lys Tyr Ile Asn Xaa Lys Leu Pro Gly Leu Leu
            565   570   575

Glu Leu Glu Tyr Glu Gly Phe Tyr Xaa Arg Gly Phe Phe Val Thr Lys
        580   585   590

Lys Xaa Tyr Ala Xaa Ile Asp Glu Glu Gly Lys Xaa Ile Thr Arg Gly
    595   600   605

Leu Glu Ile Val Arg Arg Asp Trp Ser Glu Ile Ala Lys Glu Thr Gln
    610   615   620

Ala Xaa Val Leu Glu Xaa Ile Leu Lys His Gly Xaa Val Glu Glu Ala
625   630   635   640

Val Xaa Ile Val Lys Glu Val Xaa Xaa Lys Leu Xaa Xaa Tyr Glu Ile
            645   650   655

Pro Pro Glu Lys Leu Xaa Ile Tyr Glu Gln Ile Thr Arg Pro Leu His
        660   665   670

Glu Tyr Lys Ala Ile Gly Pro His Val Ala Val Ala Lys Xaa Leu Ala
    675   680   685

Ala Xaa Gly Val Lys Xaa Xaa Pro Gly Met Val Ile Gly Tyr Ile Val
    690   695   700

Leu Arg Gly Asp Gly Pro Ile Ser Xaa Arg Ala Ile Leu Ala Glu Glu
705   710   715   720

Xaa Asp Xaa Xaa Lys His Lys Tyr Asp Ala Glu Tyr Tyr Ile Glu Asn
            725   730   735

Gln Val Leu Pro Ala Val Leu Arg Ile Leu Glu Xaa Phe Gly Tyr Arg
            740   745   750

56

Lys Glu Asp Leu Arg Xaa Gln Lys Thr Xaa Gln Xaa Gly Leu Thr Xaa
        755   760   765

Trp Leu Asn Ile Lys Lys Ser Gly Thr His Asn Cys Asn His Asp
    770   775   780

<210> 27
<211> 845
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:hybrid
      polymerase HyS1 from Figure 11

<220>
<221> MOD_RES
<222> (472)
<223> Xaa = unknown amino acid

<400> 27
Met Ile Leu Asp Ala Asp Tyr Ile Thr Glu Asp Gly Lys Pro Val Ile
  1   5   10   15

Arg Leu Phe Lys Lys Glu Asn Gly Glu Phe Lys Ile Glu Tyr Asp Arg
            20   25   30

Thr Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Arg Asp Asp Ser Lys Ile
        35   40   45

Glu Glu Val Arg Lys Ile Thr Ala Glu Arg His Gly Lys Ile Val Arg
    50   55   60

Ile Val Asp Val Glu Lys Val Arg Lys Lys Phe Leu Gly Arg Pro Ile
 65   70   75   80

Lys Val Trp Arg Leu Tyr Phe Glu His Pro Gln Asp Val Pro Thr Ile
            85   90   95

Arg Asp Lys Val Arg Glu His Pro Ala Val Ile Asp Ile Phe Glu Tyr
            100   105   110

Asp Ile Ala Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro
        115   120   125

Met Glu Gly Glu Glu Glu Leu Lys Ile Leu Ala Phe Asp Ile Glu Thr
    130   135   140

Leu Tyr His Gly Ser Glu Glu Phe Gly Lys Gly Pro Ile Ile Met Ile
145   150   155   160

Ser Tyr Ala Asp Glu Asn Glu Ala Lys Val Ile Thr Trp Lys Asn Ile
            165   170   175

Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile Lys
        180   185   190

Arg Phe Leu Arg Ile Ile Arg Glu Lys Asp Pro Asp Ile Ile Val Thr
        195   200   205

```
Tyr Asn Gly Asp Ser Phe Asp Leu Pro Tyr Leu Ala Lys Arg Ala Glu
    210             215             220
Lys Leu Gly Ile Lys Leu Thr Leu Gly Arg Asp Gly Cys Glu Ala Lys
225             230             235             240
Met Gln Arg Leu Gly Asp Met Thr Ala Val Glu Val Lys Gly Arg Ile
            245             250             255
His Phe Asp Leu Tyr Tyr Val Ile Ser Arg Thr Ile Asn Leu Pro Thr
            260             265             270
Tyr Thr Leu Glu Ala Val Tyr Glu Ala Ile Phe Gly Lys Pro Lys Glu
            275             280             285
Lys Val Tyr Ala Asp Asp Ile Ala Glu Ala Trp Glu Thr Gly Lys Gly
    290             295             300
Leu Glu Arg Val Ala Lys Tyr Ser Met Glu Asp Ala Lys Ala Thr Tyr
305             310             315             320
Glu Leu Gly Lys Glu Phe Leu Pro Met Glu Ala Gln Leu Ser Arg Leu
            325             330             335
Val Gly Gln Pro Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu
            340             345             350
Val Glu Trp Tyr Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Val Ala
            355             360             365
Pro Asn Lys Pro Tyr Glu Arg Glu Tyr Glu Arg Arg Leu Arg Glu Ser
    370             375             380
Tyr Thr Gly Gly Phe Val Lys Glu Pro Glu Lys Gly Leu Trp Glu Ser
385             390             395             400
Leu Val Ser Leu Asp Phe Arg Ser Leu Tyr Pro Ser Ile Ile Ile Thr
            405             410             415
His Asn Val Ser Pro Asp Thr Leu Asn Arg Glu Gly Cys Lys Asp Tyr
            420             425             430
Asp Ile Ala Pro Glu Val Gly His Lys Phe Cys Lys Asp Phe Leu Gly
    435             440             445
Phe Ile Pro Ser Leu Leu Gly His Leu Leu Glu Glu Arg Gln Glu Ile
    450             455             460
Lys Thr Lys Met Lys Glu Thr Xaa Asp Pro Ile Glu Lys Ile Leu Leu
465             470             475             480
Asp Tyr Arg Gln Lys Ala Ile Lys Leu Leu Ala Asn Ser Tyr Tyr Gly
            485             490             495
Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu
            500             505             510
Ser Val Thr Ala Trp Gly Arg Glu Tyr Ile Glu Phe Val Trp Lys Glu
            515             520             525
```

58

```
Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ile Asp Thr Asp Gly
    530             535             540

Leu Tyr Ala Thr Ile Pro Gly Gly Glu Pro Glu Glu Ile Lys Lys Lys
545             550             555             560

Ala Leu Glu Phe Val Lys Tyr Ile Asn Ser Lys Leu Pro Gly Leu Leu
                565             570             575

Glu Leu Glu Tyr Glu Gly Phe Tyr Lys Arg Gly Phe Phe Val Thr Lys
            580             585             590

Lys Arg Tyr Ala Val Ile Asp Glu Glu Gly Lys Ile Ile Thr Arg Gly
        595             600             605

Leu Glu Ile Val Arg Arg Asp Trp Ser Glu Ile Ala Lys Glu Thr Gln
    610             615             620

Ala Lys Val Leu Glu Ala Ile Leu Lys His Gly Asn Val Glu Glu Ala
625             630             635             640

Val Lys Ile Val Lys Glu Ile Ile Glu Lys Leu Ala Lys Tyr Glu Ile
            645             650             655

Pro Pro Glu Lys Leu Ala Ile Tyr Glu Gln Ile Thr Arg Pro Leu His
        660             665             670

Glu Tyr Lys Ala Ile Gly Pro His Val Ala Val Ala Lys Lys Leu Ala
    675             680             685

Ala Arg Gly Val Lys Ile Lys Pro Gly Met Val Ile Gly Tyr Ile Val
    690             695             700

Leu Arg Gly Asp Gly Pro Ile Ser Lys Arg Ala Ile Leu Ala Glu Glu
705             710             715             720

Phe Asp Pro Lys Lys His Lys Tyr Asp Ala Glu Tyr Tyr Ile Glu Asn
            725             730             735

Gln Val Leu Pro Ala Val Leu Arg Ile Leu Glu Gly Phe Gly Tyr Arg
        740             745             750

Lys Glu Asp Leu Arg Trp Gln Lys Thr Lys Gln Ala Gly Leu Thr Ala
        755             760             765

Trp Leu Asn Ile Lys Lys Ser Gly Thr Gly Gly Gly Ala Thr Val
770             775             780

Lys Phe Lys Tyr Lys Gly Glu Glu Lys Glu Val Asp Ile Ser Lys Ile
785             790             795             800

Lys Lys Val Trp Arg Val Gly Lys Met Ile Ser Phe Thr Tyr Asp Glu
            805             810             815

Gly Gly Gly Lys Thr Gly Arg Gly Ala Val Ser Glu Lys Asp Ala Pro
        820             825             830

Lys Glu Leu Leu Gln Met Leu Glu Lys Gln Lys Lys Asn
    835             840             845
```

59

<210> 28
<211> 758
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:hybrid
      polymerase Hyb2 from Figure 11

<220>
<221> MOD_RES
<222> (472)
<223> Xaa = unknown amino acid

<400> 28
Met Ile Leu Asp Ala Asp Tyr Ile Thr Glu Glu Gly Lys Pro Val Ile
  1   5   10   15

Arg Ile Phe Lys Lys Glu Asn Gly Glu Phe Lys Val Glu Tyr Asp Arg
                20   25   30

Asn Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Glu Asp Asp Ser Lys Ile
            35   40   45

Asp Glu Val Arg Lys Ile Thr Ala Glu Arg His Gly Lys Ile Val Arg
     50   55   60

Ile Val Asp Ala Glu Lys Val Glu Lys Lys Phe Leu Gly Arg Pro Ile
 65   70   75   80

Thr Val Trp Lys Leu Tyr Phe Glu His Pro Gln Asp Val Pro Thr Ile
                85   90   95

Arg Glu Lys Ile Arg Glu His Ser Ala Val Val Gly Ile Phe Glu Tyr
               100   105   110

Asp Ile Pro Phe Ala Lys Ser Tyr Leu Ile Asp Lys Gly Leu Ile Pro
           115   120   125

Met Glu Gly Glu Glu Glu Leu Lys Leu Leu Ala Phe Asp Ile Glu Thr
       130   135   140

Leu Tyr His Glu Gly Glu Glu Phe Ala Lys Gly Pro Ile Ile Met Ile
145   150   155   160

Ser Tyr Ala Asp Glu Asp Glu Ala Lys Val Ile Thr Trp Lys Lys Ile
               165   170   175

Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile Lys
           180   185   190

Arg Phe Leu Arg Val Ile Arg Glu Lys Asp Pro Asp Val Ile Val Thr
           195   200   205

Tyr Asn Gly Asp Ser Phe Asp Leu Pro Tyr Leu Ala Lys Arg Ala Glu
       210   215   220

Lys Leu Gly Ile Lys Leu Pro Leu Gly Arg Asp Gly Ser Glu Pro Lys
225   230   235   240

60

```
Met Gln Arg Leu Gly Asp Met Thr Ala Val Glu Val Lys Gly Arg Ile
            245                 250                 255

His Phe Asp Leu Tyr His Val Ile Ser Arg Thr Ile Asn Leu Pro Thr
            260                 265                 270

Tyr Thr Leu Glu Ala Val Tyr Glu Ala Ile Phe Gly Lys Pro Lys Glu
        275                 280                 285

Lys Val Tyr Ala Asp Glu Ile Ala Gly Ala Trp Glu Thr Gly Glu Asp
        290                 295                 300

Leu Glu Arg Val Ala Lys Tyr Ser Met Glu Asp Ala Lys Ala Ile Tyr
305                 310                 315                 320

Glu Leu Gly Lys Glu Phe Phe Pro Met Glu Val Gln Leu Pro Arg Leu
            325                 330                 335

Val Gly Gln Pro Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu
            340                 345                 350

Val Glu Trp Leu Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Leu Ala
            355                 360                 365

Pro Asn Lys Pro Ala Glu Gln Glu Tyr Glu Arg Arg Leu Arg Glu Ser
    370                 375                 380

Tyr Thr Gly Gly Phe Val Lys Glu Pro Glu Lys Gly Leu Trp Glu Asp
385                 390                 395                 400

Leu Val Ser Leu Asp Phe Arg Ala Leu Tyr Pro Ser Ile Ile Ile Thr
                405                 410                 415

His Asn Val Ser Pro Asp Thr Leu Asn Arg Glu Gly Cys Lys Asp Tyr
            420                 425                 430

Asp Ile Ala Pro Glu Val Gly His Lys Phe Cys Lys Asp Phe Leu Gly
        435                 440                 445

Phe Ile Pro Ser Leu Leu Gly His Leu Leu Glu Glu Arg Gln Glu Ile
    450                 455                 460

Lys Thr Lys Met Lys Glu Thr Xaa Asp Pro Ile Glu Lys Ile Leu Leu
465                 470                 475                 480

Asp Tyr Arg Gln Lys Ala Ile Lys Leu Leu Ala Asn Ser Tyr Tyr Gly
            485                 490                 495

Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu
        500                 505                 510

Ser Val Thr Ala Trp Gly Arg Glu Tyr Ile Glu Phe Val Trp Lys Glu
        515                 520                 525

Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ile Asp Thr Asp Gly
    530                 535                 540

Leu Tyr Ala Thr Ile Pro Gly Gly Glu Pro Glu Glu Ile Lys Lys Lys
545                 550                 555                 560
```

61

```
Ala Leu Glu Phe Val Lys Tyr Ile Asn Ser Lys Leu Pro Gly Leu Leu
                565             570             575

Glu Leu Glu Tyr Glu Gly Phe Tyr Lys Arg Gly Phe Phe Val Thr Lys
            580             585             590

Lys Arg Tyr Ala Val Ile Asp Glu Glu Gly Lys Ile Ile Thr Arg Gly
        595             600             605

Leu Glu Ile Val Arg Arg Asp Trp Ser Glu Ile Ala Lys Glu Thr Gln
    610             615             620

Ala Lys Val Leu Glu Ala Ile Leu Lys His Gly Asn Val Glu Glu Ala
625             630             635             640

Val Lys Ile Val Lys Glu Ile Ile Glu Lys Leu Ala Lys Tyr Glu Ile
            645             650             655

Pro Pro Glu Lys Leu Ala Ile Tyr Glu Gln Ile Thr Arg Pro Leu His
            660             665             670

Glu Tyr Lys Ala Ile Gly Pro His Val Ala Val Ala Lys Lys Leu Ala
        675             680             685

Ala Arg Gly Val Lys Ile Lys Pro Gly Met Val Ile Gly Tyr Ile Val
    690             695             700

Leu Arg Gly Asp Gly Pro Ile Ser Asn Arg Ala Ile Leu Ala Glu Glu
705             710             715             720

Phe Asp Leu Arg Lys His Lys Tyr Asp Ala Glu Tyr Tyr Ile Glu Asn
            725             730             735

Gln Val Leu Pro Ala Val Leu Arg Ile Leu Glu Gly Phe Gly Tyr Arg
            740             745             750

Lys Glu Asp Leu Arg Asn
            755


<210> 29
<211> 758
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:hybrid
      polymerase Hyb3 from Figure 11

<220>
<221> MOD_RES
<222> (472)
<223> Xaa = unknown amino acid

<400> 29
Met Ile Leu Asp Ala Asp Tyr Ile Thr Glu Glu Gly Lys Pro Val Ile
  1             5               10              15

Arg Ile Phe Lys Lys Glu Asn Gly Glu Phe Lys Val Glu Tyr Asp Arg
            20              25              30
```

Asn Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Glu Asp Asp Ser Lys Ile
        35   40   45

Asp Glu Val Arg Lys Ile Thr Ala Glu Arg His Gly Lys Ile Val Arg
    50   55   60

Ile Val Asp Ala Glu Lys Val Glu Lys Lys Phe Leu Gly Arg Pro Ile
65   70   75   80

Thr Val Trp Lys Leu Tyr Phe Glu His Pro Gln Asp Val Pro Thr Ile
            85   90   95

Arg Glu Lys Ile Arg Glu His Ser Ala Val Val Gly Ile Phe Glu Tyr
            100   105   110

Asp Ile Pro Phe Ala Lys Ser Tyr Leu Ile Asp Lys Gly Leu Ile Pro
        115   120   125

Met Glu Gly Glu Glu Glu Leu Lys Leu Leu Ala Phe Asp Ile Glu Thr
    130   135   140

Leu Tyr His Glu Gly Glu Glu Phe Ala Lys Gly Pro Ile Ile Met Ile
145   150   155   160

Ser Tyr Ala Asp Glu Asp Glu Ala Lys Val Ile Thr Trp Lys Lys Ile
            165   170   175

Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile Lys
        180   185   190

Arg Phe Leu Arg Val Ile Arg Glu Lys Asp Pro Asp Val Ile Val Thr
        195   200   205

Tyr Asn Gly Asp Ser Phe Asp Leu Pro Tyr Leu Ala Lys Arg Ala Glu
    210   215   220

Lys Leu Gly Ile Lys Leu Pro Leu Gly Arg Asp Gly Ser Glu Pro Lys
225   230   235   240

Met Gln Arg Leu Gly Asp Met Thr Ala Val Glu Val Lys Gly Arg Ile
            245   250   255

His Phe Asp Leu Tyr His Val Ile Ser Arg Thr Ile Asn Leu Pro Thr
        260   265   270

Tyr Thr Leu Glu Ala Val Tyr Glu Ala Ile Phe Gly Lys Pro Lys Glu
        275   280   285

Lys Val Tyr Ala Asp Glu Ile Ala Gly Ala Trp Glu Thr Gly Glu Asp
    290   295   300

Leu Glu Arg Val Ala Lys Tyr Ser Met Glu Asp Ala Lys Ala Ile Tyr
305   310   315   320

Glu Leu Gly Lys Glu Phe Phe Pro Met Glu Val Gln Leu Pro Arg Leu
            325   330   335

Val Gly Gln Pro Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu
            340   345   350

63

Val Glu Trp Leu Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Leu Ala
        355   360   365

Pro Asn Lys Pro Ala Glu Gln Glu Tyr Glu Arg Arg Leu Arg Glu Ser
    370   375   380

Tyr Thr Gly Gly Phe Val Lys Glu Pro Glu Lys Gly Leu Trp Glu Asp
385   390   395   400

Leu Val Ser Leu Asp Phe Arg Ala Leu Tyr Pro Ser Ile Ile Ile Thr
            405   410   415

His Asn Val Ser Pro Asp Thr Leu Asn Arg Glu Gly Cys Lys Asp Tyr
            420   425   430

Asp Ile Ala Pro Glu Val Gly His Lys Phe Cys Lys Asp Phe Leu Gly
        435   440   445

Phe Ile Pro Ser Leu Leu Gly His Leu Leu Glu Glu Arg Gln Glu Ile
    450   455   460

Lys Thr Lys Met Lys Glu Thr Xaa Asp Pro Ile Glu Lys Ile Leu Leu
465   470   475   480

Asp Tyr Arg Gln Lys Ala Ile Lys Leu Leu Ala Asn Ser Tyr Tyr Gly
            485   490   495

Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu
        500   505   510

Ser Val Thr Ala Trp Gly Arg Glu Tyr Ile Glu Phe Val Trp Lys Glu
        515   520   525

Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ile Asp Thr Asp Gly
    530   535   540

Leu Tyr Ala Thr Ile Pro Gly Gly Glu Pro Glu Glu Ile Lys Lys Lys
545   550   555   560

Ala Leu Glu Phe Val Lys Tyr Ile Asn Ser Lys Leu Pro Gly Leu Leu
            565   570   575

Glu Leu Glu Tyr Glu Gly Phe Tyr Lys Arg Gly Phe Phe Val Thr Lys
        580   585   590

Lys Arg Tyr Ala Val Ile Asp Glu Glu Gly Lys Ile Ile Thr Arg Gly
        595   600   605

Leu Glu Ile Val Arg Arg Asp Trp Ser Glu Ile Ala Lys Glu Thr Gln
    610   615   620

Ala Lys Val Leu Glu Ala Ile Leu Lys His Gly Asn Val Glu Glu Ala
625   630   635   640

Val Lys Ile Val Lys Glu Ile Ile Glu Lys Leu Ala Lys Tyr Glu Ile
            645   650   655

Pro Pro Glu Lys Leu Ala Ile Tyr Glu Gln Ile Thr Arg Pro Leu His
        660   665   670

```
Glu Tyr Lys Ala Ile Gly Pro His Val Ala Val Ala Lys Lys Leu Ala
        675             680             685

Ala Arg Gly Val Lys Ile Lys Pro Gly Met Val Ile Gly Tyr Ile Val
        690             695             700

Leu Arg Gly Asp Gly Pro Ile Ser Asn Arg Ala Ile Leu Ala Glu Glu
705             710             715             720

Phe Asp Leu Arg Lys His Lys Tyr Asp Ala Glu Tyr Tyr Ile Glu Asn
            725             730             735

Gln Val Leu Pro Ala Val Leu Arg Ile Leu Glu Gly Phe Gly Tyr Arg
            740             745             750

Lys Glu Asp Leu Arg Asn
        755
```


```
<210> 30
<211> 845
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:hybrid
      polymerase HyS4 from Figure 11

<220>
<221> MOD_RES
<222> (472)
<223> Xaa = unknown amino acid

<400> 30
Met Ile Leu Asp Ala Asp Tyr Ile Thr Glu Glu Gly Lys Pro Val Ile
  1             5             10                15

Arg Ile Phe Lys Lys Glu Asn Gly Glu Phe Lys Val Glu Tyr Asp Arg
            20             25             30

Asn Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Glu Asp Asp Ser Lys Ile
        35             40             45

Asp Glu Val Arg Lys Ile Thr Ala Glu Arg His Gly Lys Ile Val Arg
    50             55             60

Ile Val Asp Ala Glu Lys Val Glu Lys Lys Phe Leu Gly Arg Pro Ile
65             70             75             80

Thr Val Trp Lys Leu Tyr Phe Glu His Pro Gln Asp Val Pro Thr Ile
            85             90             95

Arg Glu Lys Ile Arg Glu His Ser Ala Val Val Gly Ile Phe Glu Tyr
            100            105            110

Asp Ile Pro Phe Ala Lys Ser Tyr Leu Ile Asp Lys Gly Leu Ile Pro
        115            120            125

Met Glu Gly Glu Glu Glu Leu Lys Leu Leu Ala Phe Asp Ile Glu Thr
    130            135            140
```

65

```
Leu Tyr His Glu Gly Glu Glu Phe Ala Lys Gly Pro Ile Ile Met Ile
145             150             155                 160

Ser Tyr Ala Asp Glu Asp Glu Ala Lys Val Ile Thr Trp Lys Lys Ile
                165             170                 175

Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile Lys
                180             185             190

Arg Phe Leu Arg Val Ile Arg Glu Lys Asp Pro Asp Val Ile Val Thr
            195             200             205

Tyr Asn Gly Asp Ser Phe Asp Leu Pro Tyr Leu Ala Lys Arg Ala Glu
    210             215             220

Lys Leu Gly Ile Lys Leu Pro Leu Gly Arg Asp Gly Ser Glu Pro Lys
225             230             235                 240

Met Gln Arg Leu Gly Asp Met Thr Ala Val Glu Val Lys Gly Arg Ile
            245             250             255

His Phe Asp Leu Tyr His Val Ile Ser Arg Thr Ile Asn Leu Pro Thr
            260             265             270

Tyr Thr Leu Glu Ala Val Tyr Glu Ala Ile Phe Gly Lys Pro Lys Glu
            275             280             285

Lys Val Tyr Ala Asp Glu Ile Ala Gly Ala Trp Glu Thr Gly Glu Asp
    290             295             300

Leu Glu Arg Val Ala Lys Tyr Ser Met Glu Asp Ala Lys Ala Ile Tyr
305             310             315                 320

Glu Leu Gly Lys Glu Phe Phe Pro Met Glu Val Gln Leu Pro Arg Leu
            325             330             335

Val Gly Gln Pro Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu
            340             345             350

Val Glu Trp Leu Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Leu Ala
            355             360             365

Pro Asn Lys Pro Ala Glu Gln Glu Tyr Glu Arg Arg Leu Arg Glu Ser
    370             375             380

Tyr Thr Gly Gly Phe Val Lys Glu Pro Glu Lys Gly Leu Trp Glu Asp
385             390             395                 400

Leu Val Ser Leu Asp Phe Arg Ala Leu Tyr Pro Ser Ile Ile Ile Thr
            405             410             415

His Asn Val Ser Pro Asp Thr Leu Asn Arg Glu Gly Cys Lys Asp Tyr
            420             425             430

Asp Ile Ala Pro Glu Val Gly His Lys Phe Cys Lys Asp Phe Leu Gly
            435             440             445

Phe Ile Pro Ser Leu Leu Gly His Leu Leu Glu Glu Arg Gln Glu Ile
    450             455             460
```

66

```
Lys Thr Lys Met Lys Glu Thr Xaa Asp Pro Ile Glu Lys Ile Leu Leu
465             470             475             480

Asp Tyr Arg Gln Lys Ala Ile Lys Leu Leu Ala Asn Ser Tyr Tyr Gly
                485             490             495

Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu
            500             505             510

Ser Val Thr Ala Trp Gly Arg Glu Tyr Ile Glu Phe Val Trp Lys Glu
        515             520             525

Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ile Asp Thr Asp Gly
    530             535             540

Leu Tyr Ala Thr Ile Pro Gly Gly Glu Pro Glu Glu Ile Lys Lys Lys
545             550             555             560

Ala Leu Glu Phe Val Lys Tyr Ile Asn Ser Lys Leu Pro Gly Leu Leu
            565             570             575

Glu Leu Glu Tyr Glu Gly Phe Tyr Lys Arg Gly Phe Phe Val Thr Lys
        580             585             590

Lys Arg Tyr Ala Val Ile Asp Glu Glu Gly Lys Ile Ile Thr Arg Gly
        595             600             605

Leu Glu Ile Val Arg Arg Asp Trp Ser Glu Ile Ala Lys Glu Thr Gln
    610             615             620

Ala Lys Val Leu Glu Ala Ile Leu Lys His Gly Asn Val Glu Glu Ala
625             630             635             640

Val Lys Ile Val Lys Glu Ile Ile Glu Lys Leu Ala Lys Tyr Glu Ile
            645             650             655

Pro Pro Glu Lys Leu Ala Ile Tyr Glu Gln Ile Thr Arg Pro Leu His
        660             665             670

Glu Tyr Lys Ala Ile Gly Pro His Val Ala Val Ala Lys Lys Leu Ala
        675             680             685

Ala Arg Gly Val Lys Ile Lys Pro Gly Met Val Ile Gly Tyr Ile Val
    690             695             700

Leu Arg Gly Asp Gly Pro Ile Ser Lys Arg Ala Ile Leu Ala Glu Glu
705             710             715             720

Phe Asp Pro Lys Lys His Lys Tyr Asp Ala Glu Tyr Tyr Ile Glu Asn
            725             730             .735

Gln Val Leu Pro Ala Val Leu Arg Ile Leu Glu Gly Phe Gly Tyr Arg
            740             745             750

Lys Glu Asp Leu Arg Trp Gln Lys Thr Lys Gln Ala Gly Leu Thr Ala
        755             760             765

Trp Leu Asn Ile Lys Lys Ser Gly Thr Gly Gly Gly Ala Thr Val
770             775             780
```

67

```
Lys Phe Lys Tyr Lys Gly Glu Glu Lys Glu Val Asp Ile Ser Lys Ile
785             790             795             800

Lys Lys Val Trp Arg Val Gly Lys Met Ile Ser Phe Thr Tyr Asp Glu
            805             810             815

Gly Gly Gly Lys Thr Gly Arg Gly Ala Val Ser Glu Lys Asp Ala Pro
            820             825             830

Lys Glu Leu Leu Gln Met Leu Glu Lys Gln Lys Lys Asn
        835             840             845


<210> 31
<211> 845
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:hybrid
      polymerase PhS1 from Figure 11

<400> 31
Met Ile Leu Asp Ala Asp Tyr Ile Thr Glu Glu Gly Lys Pro Val Ile
  1             5               10              15

Arg Leu Phe Lys Lys Glu Asn Gly Glu Phe Lys Ile Glu His Asp Arg
            20              25              30

Thr Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Lys Asp Asp Ser Lys Ile
        35              40              45

Glu Glu Val Lys Lys Ile Thr Ala Glu Arg His Gly Lys Ile Val Arg
    50              55              60

Ile Val Asp Ala Glu Lys Val Glu Lys Lys Phe Leu Gly Arg Pro Ile
 65             70              75              80

Thr Val Trp Arg Leu Tyr Phe Glu His Pro Gln Asp Val Pro Thr Ile
            85              90              95

Arg Glu Lys Ile Arg Glu His Ser Ala Val Val Asp Ile Phe Glu Tyr
            100             105             110

Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro
        115             120             125

Met Glu Gly Asp Glu Glu Leu Lys Leu Leu Ala Phe Asp Ile Glu Thr
    130             135             140

Leu Tyr His Glu Gly Glu Glu Phe Gly Lys Gly Pro Ile Ile Met Ile
145             150             155             160

Ser Tyr Ala Asp Glu Glu Glu Ala Lys Val Ile Thr Trp Lys Lys Ile
            165             170             175

Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile Lys
        180             185             190

Arg Phe Leu Lys Ile Ile Arg Glu Lys Asp Pro Asp Ile Ile Ile Thr
        195             200             205
```

68

```
Tyr Asn Gly Asp Ser Phe Asp Leu Pro Tyr Leu Ala Lys Arg Ala Glu
    210             215             220

Lys Leu Gly Ile Lys Leu Thr Ile Gly Arg Asp Gly Ser Glu Pro Lys
225             230             235                 240

Met Gln Arg Ile Gly Asp Met Thr Ala Val Glu Val Lys Gly Arg Ile
            245             250             255

His Phe Asp Leu Tyr His Val Ile Arg Arg Thr Ile Asn Leu Pro Thr
            260             265             270

Tyr Thr Leu Glu Ala Val Tyr Glu Ala Ile Phe Gly Lys Pro Lys Glu
        275             280             285

Lys Val Tyr Ala Asp Glu Ile Ala Lys Ala Trp Glu Thr Gly Glu Gly
    290             295             300

Leu Glu Arg Val Ala Lys Tyr Ser Met Glu Asp Ala Lys Ala Thr Tyr
305             310             315             320

Glu Leu Gly Lys Glu Phe Phe Pro Met Glu Ala Gln Leu Ser Arg Leu
            325             330             335

Val Gly Gln Pro Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu
            340             345             350

Val Glu Trp Phe Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Leu Ala
        355             360             365

Pro Asn Lys Pro Asp Glu Arg Glu Tyr Glu Arg Arg Leu Arg Glu Ser
    370             375             380

Tyr Ala Gly Gly Phe Val Lys Glu Pro Glu Lys Gly Leu Trp Glu Asn
385             390             395                 400

Ile Val Ser Leu Asp Phe Arg Ala Leu Tyr Pro Ser Ile Ile Ile Thr
            405             410             415

His Asn Val Ser Pro Asp Thr Leu Asn Arg Glu Gly Cys Arg Asn Tyr
            420             425             430

Asp Val Ala Pro Glu Val Gly His Lys Phe Cys Lys Asp Phe Pro Gly
        435             440             445

Phe Ile Pro Ser Leu Leu Lys Arg Leu Leu Asp Glu Arg Gln Lys Ile
    450             455             460

Lys Thr Lys Met Lys Ala Ser Gln Asp Pro Ile Glu Lys Ile Met Leu
465             470             475             480

Asp Tyr Arg Gln Arg Ala Ile Lys Ile Leu Ala Asn Ser Tyr Tyr Gly
            485             490             495

Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu
            500             505             510

Ser Val Thr Ala Trp Gly Arg Glu Tyr Ile Glu Phe Val Trp Lys Glu
            515             520             525
```

69

```
Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ile Asp Thr Asp Gly
    530             535             540

Leu Tyr Ala Thr Ile Pro Gly Gly Lys Ser Glu Glu Ile Lys Lys Lys
545             550             555                     560

Ala Leu Glu Phe Val Asp Tyr Ile Asn Ala Lys Leu Pro Gly Leu Leu
            565             570                     575

Glu Leu Glu Tyr Glu Gly Phe Tyr Lys Arg Gly Phe Phe Val Thr Lys
        580             585             590

Lys Lys Tyr Ala Leu Ile Asp Glu Glu Gly Lys Ile Ile Thr Arg Gly
        595             600             605

Leu Glu Ile Val Arg Arg Asp Trp Ser Glu Ile Ala Lys Glu Thr Gln
    610             615             620

Ala Arg Val Leu Glu Ala Ile Leu Lys His Gly Asn Val Glu Glu Ala
625             630             635                     640

Val Arg Ile Val Lys Glu Val Thr Gln Lys Leu Ser Lys Tyr Glu Ile
            645             650             655

Pro Pro Glu Lys Leu Ala Ile Tyr Glu Gln Ile Thr Arg Pro Leu His
        660             665             670

Glu Tyr Lys Ala Ile Gly Pro His Val Ala Val Ala Lys Arg Leu Ala
        675             680             685

Ala Lys Gly Val Lys Ile Lys Pro Gly Met Val Ile Gly Tyr Ile Val
        690             695             700

Leu Arg Gly Asp Gly Pro Ile Ser Asn Arg Ala Ile Leu Ala Glu Glu
705             710             715                     720

Tyr Asp Pro Arg Lys His Lys Tyr Asp Ala Glu Tyr Tyr Ile Glu Asn
            725             730             735

Gln Val Leu Pro Ala Val Leu Arg Ile Leu Glu Gly Phe Gly Tyr Arg
        740             745             750

Lys Glu Asp Leu Arg Trp Gln Lys Thr Lys Gln Thr Gly Leu Thr Ser
        755             760             765

Trp Leu Asn Ile Lys Lys Ser Gly Thr Gly Gly Gly Gly Ala Thr Val
    770             775             780

Lys Phe Lys Tyr Lys Gly Glu Glu Lys Glu Val Asp Ile Ser Lys Ile
785             790             795                     800

Lys Lys Val Trp Arg Val Gly Lys Met Ile Ser Phe Thr Tyr Asp Glu
            805             810             815

Gly Gly Gly Lys Thr Gly Arg Gly Ala Val Ser Glu Lys Asp Ala Pro
        820             825             830

Lys Glu Leu Leu Gln Met Leu Glu Lys Gln Lys Lys Asn
    835             840             845
```

70

<210> 32
<211> 845
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:hybrid
      polymerase PhS2 from Figure 11

<400> 32
Met Ile Leu Asp Val Asp Tyr Ile Thr Glu Glu Gly Lys Pro Val Ile
  1   5   10   15

Arg Leu Phe Lys Lys Glu Asn Gly Glu Phe Lys Val Glu Tyr Asp Arg
            20   25   30

Thr Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Lys Asp Asp Ser Lys Ile
            35   40   45

Asp Glu Val Arg Lys Ile Thr Gly Glu Arg His Gly Lys Ile Val Arg
        50   55   60

Ile Ile Asp Ala Glu Lys Val Arg Lys Lys Phe Leu Gly Lys Pro Ile
65   70   75   80

Glu Val Trp Lys Leu Tyr Phe Glu His Pro Gln Asp Val Pro Thr Ile
                85   90   95

Arg Glu Lys Ile Arg Glu His Ser Ala Val Val Asp Ile Phe Glu Tyr
            100   105   110

Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro
            115   120   125

Met Glu Gly Glu Glu Glu Leu Lys Ile Leu Ala Phe Asp Ile Glu Thr
    130   135   140

Leu Tyr His Glu Gly Glu Glu Phe Gly Lys Gly Pro Ile Ile Met Ile
145   150   155   160

Ser Tyr Ala Asp Glu Asn Glu Ala Lys Val Ile Thr Trp Lys Lys Ile
            165   170   175

Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile Lys
            180   185   190

Arg Phe Leu Lys Val Ile Arg Glu Lys Asp Pro Asp Ile Ile Val Thr
            195   200   205

Tyr Asn Gly Asp Ser Phe Asp Phe Pro Tyr Leu Ala Lys Arg Ala Glu
    210   215   220

Lys Leu Gly Ile Lys Leu Pro Ile Gly Arg Asp Gly Ser Glu Pro Lys
225   230   235   240

Met Gln Arg Ile Gly Asp Met Thr Ala Val Glu Val Lys Gly Arg Ile
            245   250   255

His Phe Asp Leu Tyr His Val Ile Arg Arg Thr Ile Asn Leu Pro Thr
            260   265   270

```
Tyr Thr Leu Glu Ala Val Tyr Glu Ala Ile Phe Gly Lys Pro Lys Glu
    275             280             285

Lys Val Tyr Ala His Glu Ile Ala Glu Ala Trp Glu Ser Gly Glu Gly
    290             295             300

Leu Glu Arg Val Ala Lys Tyr Ser Met Glu Asp Ala Lys Ala Thr Tyr
305             310             315             320

Glu Leu Gly Lys Glu Phe Phe Pro Met Glu Ile Gln Leu Ser Arg Leu
            325             330             335

Val Gly Gln Pro Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu
            340             345             350

Val Glu Trp Phe Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Leu Ala
            355             360             365

Pro Asn Lys Pro Ser Glu Arg Glu Tyr Glu Arg Arg Leu Arg Glu Ser
    370             375             380

Tyr Thr Gly Gly Tyr Val Lys Glu Pro Glu Lys Gly Leu Trp Glu Asn
385             390             395             400

Ile Val Tyr Leu Asp Phe Arg Ser Leu Tyr Pro Ser Ile Ile Ile Thr
            405             410             415

His Asn Val Ser Pro Asp Thr Leu Asn Leu Glu Gly Cys Lys Glu Tyr
            420             425             430

Asp Val Ala Pro Glu Val Gly His Lys Phe Cys Lys Asp Ile Pro Gly
            435             440             445

Phe Ile Pro Ser Leu Leu Gly His Leu Leu Glu Glu Arg Gln Lys Ile
    450             455             460

Lys Arg Lys Met Lys Ala Ser Lys Asp Pro Ile Glu Lys Ile Leu Leu
465             470             475             480

Asp Tyr Arg Gln Arg Ala Ile Lys Leu Leu Ala Asn Ser Phe Tyr Gly
            485             490             495

Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu
            500             505             510

Ser Val Thr Ala Trp Gly Arg Glu Tyr Ile Glu Leu Val Arg Lys Glu
            515             520             525

Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ile Asp Thr Asp Gly
    530             535             540

Leu Tyr Ala Thr Ile Pro Gly Gly Lys Ser Glu Glu Ile Lys Lys Lys
545             550             555             560

Ala Leu Glu Phe Val Asp Tyr Ile Asn Ser Lys Leu Pro Gly Leu Leu
            565             570             575

Glu Leu Glu Tyr Glu Gly Phe Tyr Lys Arg Gly Phe Phe Val Thr Lys
            580             585             590
```

Lys Arg Tyr Ala Leu Ile Asp Glu Glu Gly Lys Ile Ile Thr Arg Gly
        595   600   605

Leu Glu Ile Val Arg Arg Asp Trp Ser Glu Ile Ala Lys Glu Thr Gln
        610   615   620

Ala Lys Val Leu Glu Thr Ile Leu Lys His Gly Asn Val Glu Glu Ala
625   630   635   640

Val Arg Ile Val Lys Glu Val Thr Gln Lys Leu Ala Lys Tyr Glu Ile
                645   650   655

Pro Pro Glu Lys Leu Ala Ile Tyr Glu Gln Ile Thr Pro Pro Leu His
            660   665   670

Glu Tyr Lys Ala Ile Gly Pro His Val Ala Val Ala Lys Arg Leu Ala
        675   680   685

Ala Arg Gly Val Lys Ile Lys Pro Gly Met Val Ile Gly Tyr Ile Val
        690   695   700

Leu Arg Gly Asp Gly Pro Ile Ser Asn Arg Ala Ile Leu Ala Glu Glu
705   710   715   720

Tyr Asp Leu Lys Lys His Lys Tyr Asp Ala Glu Tyr Tyr Ile Glu Asn
                725   730   735

Gln Val Leu Pro Ala Val Leu Arg Ile Leu Glu Ala Phe Gly Tyr Arg
            740   745   750

Lys Glu Asp Leu Arg Tyr Gln Lys Thr Lys Gln Val Asp Leu Thr Ala
            755   760   765

Cys Leu Asn Ile Lys Lys Ser Gly Thr Gly Gly Gly Gly Ala Thr Val
        770   775   780

Lys Phe Lys Tyr Lys Gly Glu Glu Lys Glu Val Asp Ile Ser Lys Ile
785   790   795   800

Lys Lys Val Trp Arg Val Gly Lys Met Ile Ser Phe Thr Tyr Asp Glu
                805   810   815

Gly Gly Gly Lys Thr Gly Arg Gly Ala Val Ser Glu Lys Asp Ala Pro
            820   825   830

Lys Glu Leu Leu Gln Met Leu Glu Lys Gln Lys Lys Asn
        835   840   845

<210> 33
<211> 145
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:hybrid
      polymerase PhS3 from Figure 11

<400> 33
Met Ile Leu Asp Ala Asp Tyr Ile Thr Glu Glu Gly Lys Pro Ile Ile
  1   5   10   15

73

Arg Leu Phe Lys Lys Glu Asn Gly Lys Phe Lys Val Glu Tyr Asp Arg
            20   25   30

Thr Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Lys Asp Asp Ser Lys Ile
        35   40   45

Asp Glu Val Arg Lys Ile Thr Gly Glu Arg His Gly Lys Ile Val Arg
    50   55   60

Ile Val Asp Ala Glu Lys Val Glu Lys Lys Phe Leu Gly Lys Pro Ile
65   70   75   80

Glu Val Trp Lys Leu Tyr Leu Glu His Pro Gln Asp Val Pro Thr Ile
                85   90   95

Arg Glu Lys Ile Arg Glu His Ser Ala Val Val Asp Ile Phe Glu Tyr
            100   105   110

Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro
        115   120   125

Met Glu Gly Val Arg Tyr Arg Asn Pro Leu Ser Arg Arg Arg Arg Val
    130   135   140

Trp
145

<210> 34
<211> 844
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:hybrid
      polymerase PhS4 from Figure 11

<400> 34
Met Ile Leu Asp Ala Asp Tyr Ile Thr Glu Glu Gly Lys Pro Val Ile
  1   5   10   15

Arg Leu Phe Lys Lys Glu Asn Gly Glu Phe Lys Val Glu Tyr Asp Arg
            20   25   30

Asn Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Arg Asp Asp Ser Gln Ile
        35   40   45

Asp Glu Val Arg Lys Ile Thr Gly Glu Arg His Gly Lys Ile Val Arg
    50   55   60

Ile Val Asp Ala Glu Lys Val Glu Lys Lys Phe Leu Gly Arg Pro Ile
65   70   75   80

Glu Val Trp Lys Leu Tyr Leu Glu His Pro Gln Asp Val Pro Ala Ile
                85   90   95

Arg Glu Lys Val Arg Glu His Ser Ala Val Val Asp Ile Phe Glu Tyr
            100   105   110

Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro
        115   120   125

74

```
Met Glu Gly Glu Glu Glu Leu Lys Leu Leu Ala Phe Asp Ile Glu Thr
    130             135             140
```

```
Leu Tyr His Glu Gly Glu Glu Phe Ala Lys Gly Pro Ile Ile Met Ile
145             150             155             160
```

```
Ser Tyr Ala Asp Glu Asn Glu Ala Lys Val Ile Thr Trp Lys Lys Ile
            165             170             175
```

```
Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile Lys
            180             185             190
```

```
Arg Phe Leu Arg Val Ile Arg Glu Lys Asp Pro Asp Val Ile Val Thr
        195             200             205
```

```
Tyr Asn Gly Asp Ser Phe Asp Leu Pro Tyr Leu Val Lys Arg Ala Glu
    210             215             220
```

```
Lys Leu Gly Ile Lys Leu Pro Ile Gly Arg Asp Gly Ser Glu Pro Lys
225             230             235             240
```

```
Met Gln Arg Ile Gly Asp Met Thr Ala Val Glu Ile Lys Gly Arg Ile
            245             250             255
```

```
His Phe Asp Leu Tyr His Val Ile Arg Arg Thr Ile Asn Leu Pro Thr
            260             265             270
```

```
Tyr Thr Leu Glu Ala Val Tyr Glu Ala Ile Phe Gly Lys Pro Lys Glu
    275             280             285
```

```
Lys Val Tyr Ala His Glu Ile Ala Lys Ala Trp Glu Ser Gly Glu Gly
    290             295             300
```

```
Leu Glu Arg Val Ala Lys Tyr Ser Met Glu Asp Ala Lys Val Thr Tyr
305             310             315             320
```

```
Glu Leu Gly Lys Glu Phe Leu Pro Met Glu Ile Gln Leu Ser Arg Leu
            325             330             335
```

```
Val Gly Gln Pro Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu
            340             345             350
```

```
Val Glu Trp Phe Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Val Ala
            355             360             365
```

```
Pro Asn Lys Pro Ser Glu Glu Glu Tyr Glu Arg Arg Leu Arg Glu Ser
    370             375             380
```

```
Tyr Ala Gly Gly Tyr Val Lys Glu Pro Glu Lys Gly Leu Trp Glu Asn
385             390             395             400
```

```
Ile Val Ser Leu Asp Phe Arg Ser Leu Tyr Pro Ser Ile Ile Ile Thr
            405             410             415
```

```
His Asn Val Ser Pro Asp Thr Leu Asn Arg Glu Gly Cys Lys Asn Tyr
            420             425             430
```

```
Asp Ile Ala Pro Gln Val Gly His Lys Phe Cys Lys Asp Ile Pro Gly
    435             440             445
```

75

```
Phe Ile Pro Ser Leu Leu Lys His Leu Leu Asp Glu Arg Gln Lys Ile
    450               455           460

Lys Arg Lys Met Lys Glu Ser Gln Asp Pro Ile Glu Lys Lys Met Leu
465               470               475               480

Asp Tyr Arg Gln Arg Ala Ile Lys Leu Leu Ala Asn Ser Tyr Tyr Gly
            485               490               495

Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu
        500               505               510

Ser Val Thr Ala Trp Gly Arg Glu Tyr Ile Glu Phe Val Arg Lys Glu
        515               520               525

Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ile Asp Thr Gly Leu
    530               535               540

Tyr Ala Thr Ile Pro Gly Ala Lys Ser Glu Glu Ile Lys Lys Lys Ala
545               550               555               560

Leu Glu Phe Val Lys Tyr Ile Asn Ser Lys Leu Pro Gly Leu Leu Glu
                565               570               575

Leu Glu Tyr Glu Gly Phe Tyr Val Arg Gly Phe Phe Val Thr Lys Lys
            580               585               590

Arg Tyr Ala Leu Ile Asp Glu Glu Gly Lys Ile Ile Thr Arg Gly Leu
        595               600               605

Glu Ile Val Arg Arg Asp Trp Ser Glu Ile Ala Lys Glu Thr Gln Ala
    610               615               620

Arg Val Leu Glu Thr Ile Leu Lys His Gly Asn Val Glu Glu Ala Val
625               630               635               640

Arg Ile Val Lys Glu Val Thr Lys Lys Leu Ser Asn Tyr Glu Ile Pro
            645               650               655

Pro Glu Lys Leu Ala Ile Tyr Glu Gln Ile Thr Arg Pro Leu His Glu
            660               665               670

Tyr Lys Ala Ile Gly Pro His Val Ala Val Ala Lys Arg Leu Ala Ala
        675               680               685

Lys Gly Val Lys Ile Arg Pro Gly Met Val Ile Gly Tyr Ile Val Leu
    690               695·              700

Arg Gly Asp Gly Pro Ile Ser Asn Arg Ala Ile Leu Ala Glu Glu Tyr
705               710               715               720

Asp Pro Lys Lys His Lys Tyr Asp Ala Glu Tyr Tyr Ile Glu Asn Gln
            725               730               735

Val Leu Pro Ala Val Leu Arg Ile Leu Glu Ala Phe Gly Tyr Arg Lys
            740               745               750

Glu Asp Leu Arg Trp Gln Lys Thr Lys Gln Val Gly Leu Thr Ala Trp
        755               760               765
```

```
Leu Asn Ile Lys Lys Ser Gly Thr Gly Gly Gly Gly Ala Thr Val Lys
    770             775             780

Phe Lys Tyr Lys Gly Glu Glu Lys Glu Val Asp Ile Ser Lys Ile Lys
785             790             795   .                  800

Lys Val Trp Arg Val Gly Lys Met Ile Ser Phe Thr Tyr Asp Glu Gly
            805             810                  815

Gly Gly Lys Thr Gly Arg Gly Ala Val Ser Glu Lys Asp Ala Pro Lys
            820             825             830

Glu Leu Leu Gln Met Leu Glu Lys Gln Lys Lys Asn
        835             840


<210> 35
<211> 845
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:hybrid
     polymerase PhS5 from Figure 11

<400> 35
Met Ile Leu Asp Ala Asp Tyr Ile Thr Glu Asp Gly Lys Pro Ile Ile
  1             5                  10                  15

Arg Leu Phe Lys Lys Glu Asn Gly Glu Phe Lys Val Glu Tyr Asp Arg
            20             25                  30

Asn Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Arg Asp Asp Ser Gln Ile
        35             40                  45

Asp Glu Val Lys Lys Ile Thr Ala Glu Arg His Gly Lys Ile Val Arg
    50             55                  60

Ile Ile Asp Ala Glu Lys Val Glu Lys Lys Phe Leu Gly Arg Pro Ile
65             70                  75                  80

Thr Val Trp Arg Leu Tyr Phe Glu His Pro Gln Asp Val Pro Ala Ile
            85                  90          .       95

Arg Asp Lys Val Arg Glu His Pro Ala Val Val Asp Ile Phe Glu Tyr
            100            105            110

Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro
        115            120            125

Met Glu Gly Glu Glu Glu Leu Lys Leu Leu Ala Phe Asp Ile Glu Thr
    130            135            140

Leu Tyr His Glu Gly Glu Glu Phe Gly Lys Gly Pro Ile Ile Met Ile
145            150            155            160

Ser Tyr Ala Asp Glu Asn Glu Ala Lys Val Ile Thr Trp Lys Lys Ile
            165            170            175

Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile Lys
        180            185            190
```

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Arg Phe Leu Arg Val Ile Arg Glu Lys Asp Pro Asp Ile Ile Ile Thr
        195                 200             205
Tyr Asn Gly Asp Ser Phe Asp Phe Pro Tyr Leu Ala Lys Arg Ala Glu
    210             215             220
Lys Leu Gly Ile Lys Leu Pro Leu Gly Arg Asp Gly Ser Glu Pro Lys
225             230             235                 240
Met Gln Arg Ile Gly Asp Met Thr Ala Val Glu Ile Lys Gly Arg Ile
                245             250             255
His Phe Asp Leu Tyr His Val Ile Thr Arg Thr Ile Asn Leu Pro Thr
            260             265                 270
Tyr Thr Leu Glu Ala Val Tyr Glu Ala Ile Phe Gly Lys Pro Lys Glu
    275             280             285
Lys Val Tyr Ala Asp Glu Ile Ala Glu Ala Trp Glu Ser Gly Lys Asn
    290             295             300
Leu Glu Arg Val Ala Lys Tyr Ser Met Glu Asp Ala Lys Ala Thr Tyr
305             310             315                 320
Glu Leu Gly Lys Glu Phe Leu Pro Met Glu Ile Gln Leu Ser Arg Leu
            325             330             335
Val Gly Gln Pro Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu
            340             345             350
Val Glu Trp Tyr Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Val Ala
            355             360             365
Pro Asn Lys Pro Asp Glu Glu Glu Tyr Glu Arg Arg Leu Arg Glu Ser
    370             375             380
Tyr Thr Gly Gly Tyr Val Lys Glu Pro Glu Lys Gly Leu Trp Glu Asn
385             390             395                 400
Leu Val Ser Leu Asp Phe Arg Ala Leu Tyr Pro Ser Ile Ile Ile Thr
            405             410             415
His Asn Val Ser Pro Asp Thr Leu Asn Arg Glu Gly Cys Lys Glu Tyr
            420             425             430
Asp Ile Ala Pro Gln Val Gly His Lys Phe Cys Lys Asp Phe Pro Gly
            435             440             445
Phe Ile Pro Ser Leu Leu Lys His Leu Leu Asp Glu Arg Gln Glu Ile
    450             455             460
Lys Arg Lys Met Lys Ala Ser Lys Asp Pro Ile Glu Lys Lys Met Leu
465             470             475                 480
Asp Tyr Arg Gln Arg Ala Ile Lys Leu Leu Ala Asn Ser Phe Tyr Gly
                485             490             495
Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu
            500             505             510
```

Ser Val Thr Ala Trp Gly Arg Glu Tyr Ile Glu Leu Val Trp Lys Glu
        515   520   525

Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ile Asp Thr Asp Gly
    530   535   540

Leu Tyr Ala Thr Ile Pro Gly Gly Lys Pro Glu Glu Ile Lys Lys Lys
545   550   555   560

Ala Leu Glu Phe Val Lys Tyr Ile Asn Ser Lys Leu Pro Gly Leu Leu
                565   570   575

Glu Leu Glu Tyr Glu Gly Phe Tyr Val Arg Gly Phe Phe Val Thr Lys
            580   585   590

Lys Arg Tyr Ala Val Ile Asp Glu Glu Gly Lys Ile Ile Thr Arg Gly
        595   600   605

Leu Glu Ile Val Arg Arg Asp Trp Ser Glu Ile Ala Lys Glu Thr Gln
    610   615   620

Ala Arg Val Leu Glu Ala Ile Leu Lys His Gly Asn Val Glu Glu Ala
625   630   635   640

Val Lys Ile Val Lys Glu Val Thr Gln Lys Leu Ala Lys Tyr Glu Ile
                645   650   655

Pro Pro Glu Lys Leu Ala Ile Tyr Glu Gln Ile Thr Arg Pro Leu His
            660   665   670

Glu Tyr Lys Ala Ile Gly Pro His Val Ala Val Ala Lys Arg Leu Ala
        675   680   685

Ala Arg Gly Val Lys Val Arg Pro Gly Met Val Ile Gly Tyr Ile Val
    690   695   700

Leu Arg Gly Asp Gly Pro Ile Ser Asn Arg Ala Ile Leu Ala Glu Glu
705   710   715   720

Tyr Asp Leu Lys Lys His Lys Tyr Asp Ala Glu Tyr Tyr Ile Glu Asn
                725   730   735

Gln Val Leu Pro Ala Val Leu Arg Ile Leu Glu Ala Phe Gly Tyr Arg
            740   745   750

Lys Glu Asp Leu Arg Trp Gln Lys Thr Lys Gln Val Gly Leu Thr Ser
        755   760   765

Trp Leu Asn Ile Lys Lys Ser Gly Thr Gly Gly Gly Gly Ala Thr Val
    770   775   780

Lys Phe Lys Tyr Lys Gly Glu Glu Lys Glu Val Asp Ile Ser Lys Ile
785   790   795   800

Lys Lys Val Trp Arg Val Gly Lys Met Ile Ser Phe Thr Tyr Asp Glu
                805   810   815

Gly Gly Gly Lys Thr Gly Arg Gly Ala Val Ser Glu Lys Asp Ala Pro
            820   825   830

Lys Glu Leu Leu Gln Met Leu Glu Lys Gln Lys Lys Asn
        835   840   845

<210> 36
<211> 472
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:hybrid
      polymerase PhS6 from Figure 11

<400> 36
Met Ile Leu Asp Ala Asp Tyr Ile Thr Glu Asp Gly Lys Pro Ile Ile
  1   5   10   15

Arg Leu Phe Lys Lys Glu Asn Gly Glu Phe Lys Val Glu Tyr Asp Arg
            20   25   30

Asn Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Arg Asp Asp Ser Gln Ile
            35   40   45

Asp Glu Val Lys Lys Ile Thr Ala Glu Arg His Gly Lys Ile Val Arg
        50   55   60

Ile Ile Asp Ala Glu Lys Val Glu Lys Lys Phe Leu Gly Arg Pro Ile
 65   70   75   80

Thr Val Trp Arg Leu Tyr Phe Glu His Pro Gln Asp Val Pro Ala Ile
                85   90   95

Arg Asp Lys Val Arg Glu His Pro Ala Val Val Asp Ile Phe Glu Tyr
            100   105   110

Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro
            115   120   125

Met Glu Gly Glu Glu Glu Leu Lys Leu Leu Ala Phe Asp Ile Glu Thr
    130   135   140

Leu Tyr His Glu Gly Glu Glu Phe Gly Lys Gly Pro Ile Ile Met Ile
145   150   155   160

Ser Tyr Ala Asp Glu Asn Glu Ala Lys Val Ile Thr Trp Lys Lys Ile
                165   170   175

Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile Lys
            180   185   190

Arg Phe Leu Arg Val Ile Arg Glu Lys Asp Pro Asp Ile Ile Ile Thr
            195   200   205

Tyr Asn Gly Asp Ser Phe Asp Phe Pro Tyr Leu Ala Lys Arg Ala Glu
    210   215   220

Lys Leu Gly Ile Lys Leu Pro Leu Gly Arg Asp Gly Ser Glu Pro Lys
225   230   235   240

80

```
Met Gln Arg Ile Gly Asp Met Thr Ala Val Glu Ile Lys Gly Arg Ile
              245               250               255

His Phe Asp Leu Tyr His Val Ile Thr Arg Thr Ile Asn Leu Pro Thr
              260               265               270

Tyr Thr Leu Glu Ala Val Tyr Glu Ala Ile Phe Gly Lys Pro Lys Glu
              275               280               285

Lys Val Tyr Ala Asp Glu Ile Ala Glu Ala Trp Glu Ser Gly Lys Asn
        290               295               300

Leu Glu Arg Val Ala Lys Tyr Ser Met Glu Asp Ala Lys Ala Thr Tyr
305               310               315               320

Glu Leu Gly Lys Glu Phe Leu Pro Met Glu Ile Gln Leu Ser Arg Leu
              325               330               335

Val Gly Gln Pro Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu
              340               345               350

Val Glu Trp Tyr Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Val Ala
              355               360               365

Pro Asn Lys Pro Asp Glu Glu Glu Tyr Glu Arg Arg Leu Arg Glu Ser
        370               375               380

Tyr Thr Gly Gly Tyr Val Lys Glu Pro Glu Lys Gly Leu Trp Glu Asn
385               390               395               400

Leu Val Ser Leu Asp Phe Arg Ala Leu Tyr Pro Ser Ile Ile Ile Thr
              405               410               415

His Asn Val Ser Pro Asp Thr Leu Asn Arg Glu Gly Cys Lys Glu Tyr
              420               425               430

Asp Val Ala Pro Gln Val Gly His Lys Phe Cys Lys Asp Phe Pro Gly
              435               440               445

Phe Ile Pro Ser Leu Leu Lys Arg Leu Leu Glu Glu Arg Gln Lys Ile
        450               455               460

Lys Arg Lys Met Lys Ala Thr Asn
465               470
```

<210> 37
<211> 844
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:hybrid
      polymerase Sso7d fusion protein PhS7

<400> 37
```
Met Ile Leu Asp Ala Asp Tyr Ile Thr Glu Asp Gly Lys Pro Ile Ile
  1           5               10               15

Arg Leu Phe Lys Lys Glu Asn Gly Glu Phe Lys Val Glu Tyr Asp Arg
        20               25               30
```

```
Asn Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Arg Asp Asp Ser Gln Ile
        35              40                  45

Asp Glu Val Lys Lys Ile Thr Ala Glu Arg His Gly Lys Ile Val Arg
     50              55                  60

Ile Ile Asp Ala Glu Lys Val Glu Lys Lys Phe Leu Gly Arg Pro Ile
65                  70              75                      80

Thr Val Trp Arg Leu Tyr Phe Glu His Pro Gln Asp Val Pro Ala Ile
            85              90                      95

Arg Asp Lys Val Arg Glu His Pro Ala Val Val Asp Ile Phe Glu Tyr
            100             105             110

Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro
        115             120             125

Met Glu Gly Glu Glu Glu Leu Lys Leu Leu Ala Phe Asp Ile Glu Thr
    130             135             140

Leu Tyr His Glu Gly Glu Glu Phe Gly Lys Gly Pro Ile Ile Met Ile
145             150             155                     160

Ser Tyr Ala Asp Glu Asn Glu Ala Lys Val Ile Thr Trp Lys Lys Ile
            165             170             175

Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile Lys
        180             185             190

Arg Phe Leu Arg Val Ile Arg Glu Lys Asp Pro Asp Ile Ile Ile Thr
        195             200             205

Tyr Asn Gly Asp Ser Phe Asp Phe Pro Tyr Leu Ala Lys Arg Ala Glu
    210             215             220

Lys Leu Gly Ile Lys Leu Pro Leu Gly Arg Asp Gly Ser Glu Pro Lys
225             230             235                     240

Met Gln Arg Ile Gly Asp Met Thr Ala Val Glu Ile Lys Gly Arg Ile
            245             250             255

His Phe Asp Leu Tyr His Val Ile Thr Arg Thr Ile Asn Leu Pro Thr
        260             265             270

Tyr Thr Leu Glu Ala Val Tyr Glu Ala Ile Phe Gly Lys Pro Lys Glu
    275             280             285

Lys Val Tyr Ala Asp Glu Ile Ala Glu Ala Trp Glu Ser Gly Lys Asn
    290             295             300

Leu Glu Arg Val Ala Lys Tyr Ser Met Glu Asp Ala Lys Ala Thr Tyr
305             310             315             320

Glu Leu Gly Lys Glu Phe Leu Pro Met Glu Ile Gln Leu Ser Arg Leu
            325             330             335

Val Gly Gln Pro Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu
            340             345             350
```

```
Val Glu Trp Tyr Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Val Ala
    355                 360             365

Pro Asn Lys Pro Asp Glu Glu Glu Tyr Glu Arg Arg Leu Arg Glu Ser
    370             375             380

Tyr Thr Gly Gly Tyr Val Lys Glu Pro Glu Lys Gly Leu Trp Glu Asn
385             390             395                 400

Leu Val Ser Leu Asp Phe Arg Ala Leu Tyr Pro Ser Ile Ile Ile Thr
            405             410             415

His Asn Val Ser Pro Asp Thr Leu Asn Arg Glu Gly Cys Arg Asn Tyr
            420             425             430

Asp Val Ala Pro Gln Val Gly His Lys Phe Cys Lys Asp Phe Pro Gly
        435             440             445

Phe Ile Pro Ser Leu Leu Gly Arg Leu Leu Glu Glu Arg Gln Glu Ile
    450             455             460

Lys Thr Lys Met Lys Ala Thr Lys Asp Pro Ile Glu Lys Lys Leu Leu
465             470             475                 480

Asp Tyr Arg Gln Lys Ala Ile Lys Ile Leu Ala Asn Ser Phe Tyr Gly
            485             490             495

Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu
        500             505             510

Ser Val Thr Ala Trp Gly Arg Lys Tyr Ile Glu Phe Val Arg Lys Glu
        515             520             525

Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ile Asp Thr Asp Gly
    530             535             540

Leu Tyr Ala Thr Ile Pro Gly Gly Lys Pro Glu Glu Ile Lys Lys Lys
545             550             555                 560

Ala Leu Glu Phe Val Lys Tyr Ile Asn Ser Lys Leu Pro Gly Leu Leu
            565             570             575

Glu Leu Glu Tyr Glu Gly Phe Tyr Val Arg Gly Phe Phe Val Thr Lys
            580             585             590

Lys Arg Tyr Ala Val Ile Asp Glu Glu Gly Lys Ile Ile Thr Arg Gly
        595             600             605

Leu Glu Ile Val Arg Arg Asp Trp Ser Glu Ile Ala Lys Glu Thr Gln
    610             615             620

Ala Arg Val Leu Glu Ala Ile Leu Lys His Gly Asn Val Glu Glu Ala
625             630             635                 640

Val Lys Ile Val Lys Glu Val Thr Gln Lys Leu Ala Lys Tyr Glu Ile
            645             650             655

Pro Pro Glu Lys Leu Ala Ile Tyr Glu Gln Ile Thr Arg Pro Leu His
        660             665             670
```

```
Glu Tyr Lys Ala Ile Gly Pro His Val Ala Val Ala Lys Arg Leu Ala
        675             680             685

Ala Arg Gly Val Lys Val Arg Pro Gly Met Val Ile Gly Tyr Ile Val
        690             695             700

Leu Arg Gly Asp Gly Pro Ile Ser Asn Arg Ala Ile Leu Ala Glu Glu
705             710             715             720

Tyr Asp Leu Lys Lys His Lys Tyr Asp Ala Glu Tyr Tyr Ile Glu Asn
            725             730             735

Gln Val Leu Pro Ala Val Leu Arg Ile Leu Glu Ala Phe Gly Tyr Arg
            740             745             750

Lys Glu Asp Leu Arg Trp Gln Lys Thr Lys Gln Val Gly Leu Thr Ser
        755             760             765

Trp Leu Asn Ile Lys Lys Ser Gly Thr Gly Gly Gly Gly Ala Thr Val
        770             775             780

Lys Phe Lys Tyr Lys Gly Glu Glu Lys Glu Val Asp Ile Ser Lys Ile
785             790             795             800

Lys Lys Val Trp Arg Val Gly Lys Met Ile Ser Phe Thr Tyr Asp Glu
            805             810             815

Gly Gly Gly Lys Thr Gly Arg Gly Ala Val Ser Glu Lys Asp Ala Pro
            820             825             830

Lys Glu Leu Leu Gln Met Leu Glu Lys Gln Lys Lys
        835             840


<210> 38
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:6-His
      polyhistidine epitope tag, metal chelate affinity
      ligand

<400> 38
His His His His His His
  1               5


<210> 39
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:anti-DYKDDDDK
      epitope tag

<400> 39
Asp Tyr Lys Asp Asp Asp Asp Lys
  1               5
```

```
<210> 40
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Fwd 1 PCR
      primer oligonucleotide

<400> 40
ttggtaccaa gcttcatatg a                                               21


<210> 41
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Fwd 2 PCR
      primer oligonucleotide

<400> 41
ccgctgccga sctatgcgac cyctcacagc kcaggcctgg atctgcgtgc g             51


<210> 42
<211> 69
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Fwd 3 PCR
      primer oligonucleotide

<400> 42
ttccgaccgg tctgatcmtt sawattscgg awggttmtgm ggsgcagrtg ckgccgcgta 60
gcggcctgg                                                            69


<210> 43
<211> 98
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Fwd 4 PCR
      primer oligonucleotide

<400> 43
ttttgatcga trscgattat crgggcsaas tgawgrttak cstggtgaac ckgggcmasg 60
awgaakttry gattsagcsg ggcgaacgta ttgcgcag                            98


<210> 44
<211> 56
<212> DNA
<213> Artificial Sequence
```

<220>
<223> Description of Artificial Sequence:Fwd 5 PCR
      primer oligonucleotide

<400> 44
cgtggcgaag gcggctttgg ctctascggc asamagtaat gaggatccga attctt   56

<210> 45
<211> 89
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Rev A PCR
      primer oligonucleotide

<400> 45
ggtcgcatag stcggcagcg gwaawtcttk gscatgasgc rgacgcwkaa ttttcasawy 60
aaytttkytc atatgaagct tggtaccaa   89

<210> 46
<211> 83
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Rev B PCR
      primer oligonucleotide

<400> 46
gatcagaccg gtcggaayca gcrycstwtc ammcggckya akttycascg swtystyaak 60
gsmcgcacgc agatccaggc ctg   83

<210> 47
<211> 68
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Rev C PCR
      primer oligonucleotide

<400> 47
ttttatcgat crkgcccrsc gcgttcagca scrytawgcc mtktttccag sccaggccgc 60
tacgcggc   68

<210> 48
<211> 107
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Rev D PCR
      primer oligonucleotide

<400> 48
tagagccaaa gccgccttcg ccacgmtsgg tctgagaaam wtcttccacc wsawyaamtt 60
ccrccygcws caccggcrca awaaycakct gcgcaatacg ttcgccc   107

<210> 49
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Rev D PCR
      primer oligonucleotide

<400> 49
aagaattcgg atcctcatta ct   22

<210> 50
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer to
      measure exonuclease activity

<220>
<221> modified_base
<222> (1)
<223> n = t modified by 6-carboxy-fluorescein (FAM)

<220>
<221> modified_base
<222> (45)
<223> n = t amino-linked to quencher
      4-(4-dimethylaminophenylazo)benzoyl group (dabcyl,
      DAB)

<400> 50
nttttgagg tgtgtcctac acagcggagt gtaggacaca cctcn   45